

PH-1064PCT-US seq.TXT

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD.

<120> Shear Stress-Responsive Genes

<130> 1241.22

<140> US/10/089,320

<141> 2002-03-28

<150> JP 1999-280976

<151> 1999-10-01

<160> 181

<170> PatentIn Ver. 2.0

<210> 1

<211> 3817

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (440)..(1930)

<400> 1

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cggcctgccg gcggggacga cagcattgcg cctgggtgca gcagtgtgcg tctcggggaa 180
gggaagatat tttaaggcgt gtctgagcag acggggaggc ttttccaaac ccaggcagct 240
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Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr

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gac tat gac ctt atc atc att gga ggt ggc tca gga ggt ctg gca gct 520

Asp Tyr Asp Leu Ile Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala

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gct aag gag gca gcc caa tat ggc aag aag gtg atg gtc ctg gac ttt 568

Ala Lys Glu Ala Ala Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe

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gtc act ccc acc cct ctt gga act aga tgg ggt ctt gga gga aca tgt 616

Val Thr Pro Thr Pro Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys

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gtg aat gtg ggt tgc ata cct aaa aaa ctg atg cat caa gca gct ttg 664

Val Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu

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tta gga caa gcc ctg caa gac tct cga aat tat gga tgg aaa gtc gag 712

Leu Gly Gln Ala Leu Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu

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90

gag aca gtt aag cat gat tgg gac aga atg ata gaa gct gta cag aat 760

Glu Thr Val Lys His Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn

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cac att ggc tct ttg aat tgg ggc tac cga gta gct ctg cgg gag aaa 808

His Ile Gly Ser Leu Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys

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Lys Val Val Tyr Glu Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg			
125	130	135	
att aag gca aca aat aat aaa ggc aaa gaa aaa att tat tca gca gag			904
Ile Lys Ala Thr Asn Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu			
140	145	150	155
agt ttt ctc att gcc act ggt gaa aga cca cgt tac ttg ggc atc cct			952
Ser Phe Leu Ile Ala Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro			
160	165	170	
ggg gac aaa gaa tac tgc atc agc agt gat gat ctt ttc tcc ttg cct			1000
Gly Asp Lys Glu Tyr Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro			
175	180	185	
tac tgc ccg ggt aag acc ctg gtt gtt gga gca tcc tat gtc gct ttg			1048
Tyr Cys Pro Gly Lys Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu			
190	195	200	
gag tgc gct gga ttt ctt gct ggt att ggt tta ggc gtc act gtt atg			1096
Glu Cys Ala Gly Phe Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met			
205	210	215	
gtt agg tcc att ctt ctt aga gga ttt gac cag gac atg gcc aac aaa			1144
Val Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys			
220	225	230	235
att ggt gaa cac atg gaa gaa cat ggc atc aag ttt ata aga cag ttc			1192
Ile Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe			

PH-1064PCT-US seq.TXT

240	245	250	
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Val Pro Ile Lys Val Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu			
255	260	265	
aga gta gta gct cag tcc acc aat agt gag gaa atc att gaa gga gaa			1288
Arg Val Val Ala Gln Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu			
270	275	280	
tat aat acg gtg atg ctg gca ata gga aga gat gct tgc aca aga aaa			1336
Tyr Asn Thr Val Met Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys			
285	290	295	
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Ile Gly Leu Glu Thr Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys			
300	305	310	315
ata cct gtc aca gat gaa gaa cag acc aat gtg cct tac atc tat gcc			1432
Ile Pro Val Thr Asp Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala			
320	325	330	
att ggc gat ata ttg gag gat aag gtg gag ctc acc cca gtt gca atc			1480
Ile Gly Asp Ile Leu Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile			
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Gln Ala Gly Arg Leu Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val			
350	355	360	
aag tgt gac tat gaa aat gtt cca acc act gta ttt act cct ttg gaa			1576
Lys Cys Asp Tyr Glu Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu			

PH-1064PCT-US seq.TXT

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Tyr Gly Ala Cys Gly Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly			
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gaa gaa aat att gag gtt tac cat agt tac ttt tgg cca ttg gaa tgg			1672
Glu Glu Asn Ile Glu Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp			
	400	405	410
acg att ccg tca aga gat aac aac aaa tgt tat gca aaa ata atc tgt			1720
Thr Ile Pro Ser Arg Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys			
	415	420	425
aat act aaa gac aat gaa cgt gtt gtg ggc ttt cac gta ctg ggt cca			1768
Asn Thr Lys Asp Asn Glu Arg Val Val Gly Phe His Val Leu Gly Pro			
	430	435	440
aat gct gga gaa gtt aca caa ggc ttt gca gct gcg ctc aaa tgt gga			1816
Asn Ala Gly Glu Val Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly			
	445	450	455
ctg acc aaa aag cag ctg gac agc aca att gga atc cac cct gtc tgt			1864
Leu Thr Lys Lys Gln Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys			
	460	465	470
gca gag gta ttc aca aca ttg tct gtg acc aag cgc tct ggg gca agc			1912
Ala Glu Val Phe Thr Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser			
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Ile Leu Gln Ala Gly Cys			

PH-1064PCT-US seq.TXT

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PH-1064PCT-US seq.TXT

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<212> PRT

<213> Homo sapiens

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Gln	Tyr	Gly	Lys	Lys	Val	Met	Val	Leu	Asp	Phe	Val	Thr	Pro	Thr	Pro
						35								40	45
Leu	Gly	Thr	Arg	Trp	Gly	Leu	Gly	Gly	Thr	Cys	Val	Asn	Val	Gly	Cys
						50								55	60
Ile	Pro	Lys	Lys	Leu	Met	His	Gln	Ala	Ala	Leu	Leu	Gly	Gln	Ala	Leu
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PH-1064PCT-US seq.TXT

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Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys Val Val Tyr Glu
115 120 125
Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile Lys Ala Thr Asn
130 135 140
Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Ser Phe Leu Ile Ala
145 150 155 160
Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly Asp Lys Glu Tyr
165 170 175
Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr Cys Pro Gly Lys
180 185 190
Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu Cys Ala Gly Phe
195 200 205
Leu Ala Gly Ile Gly Leu Gly Val Thr Val Met Val Arg Ser Ile Leu
210 215 220
Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile Gly Glu His Met
225 230 235 240
Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val Pro Ile Lys Val
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Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg Val Val Ala Gln
260 265 270

PH-1064PCT-US seq.TXT

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290 295 300
Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile Pro Val Thr Asp
305 310 315 320
Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile Gly Asp Ile Leu
325 330 335
Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln Ala Gly Arg Leu
340 345 350
Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys Cys Asp Tyr Glu
355 360 365
Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr Gly Ala Cys Gly
370 375 380
Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu Glu Asn Ile Glu
385 390 395 400
Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr Ile Pro Ser Arg
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Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn Thr Lys Asp Asn
420 425 430
Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn Ala Gly Glu Val
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PH-1064PCT-US seq.TXT

Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala Glu Val Phe Thr
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<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (6)..(938)

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 Trp Pro Arg Pro Pro Ala Pro Gly Pro Pro Pro Pro Pro Leu Pro Leu
 20 25 30
 ctg ctc ctg ctc ctg gcc ggg ctg ctg ggc ggc gcg ggc gcg cag tac 146
 Leu Leu Leu Leu Leu Ala Gly Leu Leu Gly Gly Ala Gly Ala Gln Tyr
 35 40 45
 tcc agc gac cgg tgc agc tgg aag ggg agc ggg ctg acg cac gag gca 194

PH-1064PCT-US seq.TXT

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His	Arg	Lys	Glu	Val	Glu	Gln	Val	Tyr	Leu	Arg	Cys	Ala	Ala	Gly	Ala		
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gtg	gag	tgg	atg	tac	cca	aca	ggg	gct	ctc	atc	ggt	aac	ctg	cgg	ccc	290	
Val	Glu	Trp	Met	Tyr	Pro	Thr	Gly	Ala	Leu	Ile	Val	Asn	Leu	Arg	Pro		
		80					85					90			95		
aac	acc	ttc	tcg	cct	gcc	cgg	cac	ctg	acc	gtg	tgc	atc	agg	tcc	ttc	338	
Asn	Thr	Phe	Ser	Pro	Ala	Arg	His	Leu	Thr	Val	Cys	Ile	Arg	Ser	Phe		
					100					105					110		
acg	gac	tcc	tcg	ggg	gcc	aat	att	tat	ttg	gaa	aaa	act	gga	gaa	ctg	386	
Thr	Asp	Ser	Ser	Gly	Ala	Asn	Ile	Tyr	Leu	Glu	Lys	Thr	Gly	Glu	Leu		
					115					120					125		
aga	ctg	ctg	gta	ccg	gac	ggg	gac	ggc	agg	ccc	ggc	cgg	gtg	cag	tgt	434	
Arg	Leu	Leu	Val	Pro	Asp	Gly	Asp	Gly	Arg	Pro	Gly	Arg	Val	Gln	Cys		
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ttt	ggc	ctg	gag	cag	ggc	ggc	ctg	ttc	gtg	gag	gcc	acg	ccg	cag	cag	482	
Phe	Gly	Leu	Glu	Gln	Gly	Gly	Leu	Phe	Val	Glu	Ala	Thr	Pro	Gln	Gln		
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cac	agg	gcg	tcg	gac	ctg	cac	gag	ctg	tct	gcg	ccg	tgc	cgt	ccc	tgc	578	

PH-1064PCT-US seq.TXT

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Ser Asp Thr Glu Val Leu Leu Ala Val Cys Thr Ser Asp Phe Ala Val		
195	200	205
cga ggc tcc atc cag caa gtt acc cac gag cct gag cgg cag gac tca		674
Arg Gly Ser Ile Gln Gln Val Thr His Glu Pro Glu Arg Gln Asp Ser		
210	215	220
gcc atc cac ctg cgc gtg agc aga ctc tat cgg cag aaa agc agg gtc		722
Ala Ile His Leu Arg Val Ser Arg Leu Tyr Arg Gln Lys Ser Arg Val		
225	230	235
ttc gag ccg gtg ccc gag ggt gac ggc cac tgg cag ggg cgc gtc agg		770
Phe Glu Pro Val Pro Glu Gly Asp Gly His Trp Gln Gly Arg Val Arg		
240	245	250
255		
acg ctg ctg gag tgt ggc gtg cgg ccg ggg cat ggc gac ttc ctc ttc		818
Thr Leu Leu Glu Cys Gly Val Arg Pro Gly His Gly Asp Phe Leu Phe		
260	265	270
act ggc cac atg cac ttc ggg gag gcg cgg ctc ggc tgt gcc cca cgc		866
Thr Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg		
275	280	285
ttc aag gac ttc cag agg atg tac agg gat gcc cag gag agg ggg ctg		914
Phe Lys Asp Phe Gln Arg Met Tyr Arg Asp Ala Gln Glu Arg Gly Leu		
290	295	300
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PH-1064PCT-US seq.TXT

Asn Pro Cys Glu Val Gly Thr Asp

305

310

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<211> 311

<212> PRT

<213> Homo sapiens

<400> 4

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30

Leu Leu Leu Leu Ala Gly Leu Leu Gly Gly Ala Gly Ala Gln Tyr Ser

35

40

45

Ser Asp Arg Cys Ser Trp Lys Gly Ser Gly Leu Thr His Glu Ala His

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55

60

PH-1064PCT-US seq.TXT

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Glu	Trp	Met	Tyr	Pro	Thr	Gly	Ala	Leu	Ile	Val	Asn	Leu	Arg	Pro	Asn
				85					90					95	
Thr	Phe	Ser	Pro	Ala	Arg	His	Leu	Thr	Val	Cys	Ile	Arg	Ser	Phe	Thr
			100					105						110	
Asp	Ser	Ser	Gly	Ala	Asn	Ile	Tyr	Leu	Glu	Lys	Thr	Gly	Glu	Leu	Arg
		115				120						125			
Leu	Leu	Val	Pro	Asp	Gly	Asp	Gly	Arg	Pro	Gly	Arg	Val	Gln	Cys	Phe
	130					135						140			
Gly	Leu	Glu	Gln	Gly	Gly	Leu	Phe	Val	Glu	Ala	Thr	Pro	Gln	Gln	Asp
145				150					155						160
Ile	Gly	Arg	Arg	Thr	Thr	Gly	Phe	Gln	Tyr	Glu	Leu	Val	Arg	Arg	His
			165					170						175	
Arg	Ala	Ser	Asp	Leu	His	Glu	Leu	Ser	Ala	Pro	Cys	Arg	Pro	Cys	Ser
		180						185						190	
Asp	Thr	Glu	Val	Leu	Leu	Ala	Val	Cys	Thr	Ser	Asp	Phe	Ala	Val	Arg
		195					200					205			
Gly	Ser	Ile	Gln	Gln	Val	Thr	His	Glu	Pro	Glu	Arg	Gln	Asp	Ser	Ala
		210				215						220			
Ile	His	Leu	Arg	Val	Ser	Arg	Leu	Tyr	Arg	Gln	Lys	Ser	Arg	Val	Phe
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PH-1064PCT-US seq.TXT

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260

265

270

Gly His Met His Phe Gly Glu Ala Arg Leu Gly Cys Ala Pro Arg Phe

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Pro Cys Glu Val Gly Thr Asp

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<210> 5

<211> 2820

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (49)..(2664)

<400> 5

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Gly Ala Ala Gln Glu Leu Gln Ala Lys Leu Ala Glu Ile Gly Ala Pro

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15

atc cag ggt aat cgc gag gag ctg gtg gag cgg ctg cag agc tac acc 153

PH-1064PCT-US seq.TXT

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20					25					30					35				
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Arg	Gln	Thr	Gly	Ile	Val	Leu	Asn	Arg	Pro	Val	Leu	Arg	Gly	Glu	Asp				
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Gly	Asp	Lys	Ala	Ala	Pro	Pro	Pro	Met	Ser	Ala	Gln	Leu	Pro	Gly	Ile				
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295 300 305
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Lys Lys Lys Lys Lys Pro Gln Arg Val Arg Gly Val Ser Ser Glu Ser
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Ser Gly Asp Arg Glu Lys Asp Ser Thr Arg Ser Arg Gly Ser Asp Ser
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Lys	Pro	Glu	Ala	Pro	Lys	Leu	Ser	Lys	Lys	Lys	Leu	Arg	Arg	Met	Asn		
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His Gly Asp Leu Tyr Tyr Glu Gly Lys Glu Phe Glu Thr Arg Leu Lys	
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Lys Glu Phe Lys Phe
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485 490 495
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610 615 620

Leu Lys Ile Pro Gly Leu Asn Ser Pro Ile Pro Glu Ser Cys Ser Phe
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Lys Pro Leu Tyr Gly Asp Val Phe Gly Thr Asn Ala Ala Glu Phe Gln
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Gly Leu Ile Thr Pro Gly Gly Phe Ser Ser Val Pro Ala Gly Met Glu
725 730 735

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Val Tyr Tyr Val Ser Tyr Ala Val Phe Val Val Thr Tyr Leu Ile Leu
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Tyr Pro Gly Pro Pro Pro Pro Gly Gly Tyr Gly Gln Pro Ser Val Leu

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25

30

Pro Gly Gly Tyr Pro Ala Tyr Pro Gly Tyr Pro Gln Pro Gly Tyr Gly

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His Pro Ala Gly Tyr Pro Gln Pro Met Pro Pro Thr His Pro Met Pro

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Thr Phe Ile Arg Lys Val Tyr Ser Ile Ile Ser Val Gln Leu Leu Ile			
	100	105	110
Thr Val Ala Ile Ile Ala Ile Phe Thr Phe Val Glu Pro Val Ser Ala			
	115	120	125
Phe Val Arg Arg Asn Val Ala Val Tyr Tyr Val Ser Tyr Ala Val Phe			
	130	135	140
Val Val Thr Tyr Leu Ile Leu Ala Cys Cys Gln Gly Pro Arg Arg Arg			
145	150	155	160
Phe Pro Trp Asn Ile Ile Leu Leu Thr Leu Phe Thr Phe Ala Met Gly			
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Phe Met Thr Gly Thr Ile Ser Ser Met Tyr Gln Thr Lys Ala Val Ile			
	180	185	190
Ile Ala Met Ile Ile Thr Ala Val Val Ser Ile Ser Val Thr Ile Phe			
	195	200	205
Cys Phe Gln Thr Lys Val Asp Phe Thr Ser Cys Thr Gly Leu Phe Cys			
	210	215	220
Val Leu Gly Ile Val Leu Leu Val Thr Gly Ile Val Thr Ser Ile Val			
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Leu Tyr Phe Gln Tyr Val Tyr Trp Leu His Met Leu Tyr Ala Ala Leu			

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 Met Pro Glu Lys Arg Pro Phe Glu Arg

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Val Arg Gln Ala Thr Asn Gln Ile Val Met Asn Cys Ala Asp Ile Asp				
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Ile Ile Thr Ala Ser Tyr Ala Pro Glu Gly Asp Glu Glu Ile His Ala				
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Thr Gly Phe Asn Tyr Gln Asn Glu Asp Glu Lys Val Thr Leu Ser Phe				
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cct agt act ctg caa aca ggt acg gga acc tta aag ata gat ttt gtt	400			
Pro Ser Thr Leu Gln Thr Gly Thr Gly Thr Leu Lys Ile Asp Phe Val				
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Gly Glu Leu Asn Asp Lys Met Lys Gly Phe Tyr Arg Ser Lys Tyr Thr				
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acc cct tct gga gag gtg cgc tat gct gct gta aca cag ttt gag gct	496			
Thr Pro Ser Gly Glu Val Arg Tyr Ala Ala Val Thr Gln Phe Glu Ala				
125	130	135		
act gat gcc cga agg gct ttt cct tgc tgg gat gag cct gct atc aaa	544			
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tca aac atg aat gta att gac cgg aaa cca tac cct gat gat gaa aat			640
Ser Asn Met Asn Val Ile Asp Arg Lys Pro Tyr Pro Asp Asp Glu Asn			
170	175	180	185
tta gtg gaa gtg aag ttt gcc cgc aca cct gtt atg tct aca tat ctg			688
Leu Val Glu Val Lys Phe Ala Arg Thr Pro Val Met Ser Thr Tyr Leu			
	190	195	200
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Val Ala Phe Val Val Gly Glu Tyr Asp Phe Val Glu Thr Arg Ser Lys			
205	210	215	
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Asp Gly Val Cys Val Arg Val Tyr Thr Pro Val Gly Lys Ala Glu Gln			
220	225	230	
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Gly Lys Phe Ala Leu Glu Val Ala Ala Lys Thr Leu Pro Phe Tyr Lys			
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gac tac ttc aat gtt cct tat cct cta cct aaa att gat ctc att gct			880
Asp Tyr Phe Asn Val Pro Tyr Pro Leu Pro Lys Ile Asp Leu Ile Ala			
250	255	260	265
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Ile Ala Asp Phe Ala Ala Gly Ala Met Glu Asn Trp Gly Leu Val Thr			

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tcc cgc cag tgg gtt gct ctg gtt gtg gga cat gaa ctc gcc cat caa			1024
Ser Arg Gln Trp Val Ala Leu Val Val Gly His Glu Leu Ala His Gln			
300	305	310	
tgg ttt gga aat ctt gtt act atg gaa tgg tgg act cat ctt tgg tta			1072
Trp Phe Gly Asn Leu Val Thr Met Glu Trp Trp Thr His Leu Trp Leu			
315	320	325	
aat gaa ggt ttt gca tcc tgg att gaa tat ctg tgt gta gac cac tgc			1120
Asn Glu Gly Phe Ala Ser Trp Ile Glu Tyr Leu Cys Val Asp His Cys			
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Phe Pro Glu Tyr Asp Ile Trp Thr Gln Phe Val Ser Ala Asp Tyr Thr			
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cgt gcc cag gag ctt gac gcc tta gat aac agc cat cct att gaa gtc			1216
Arg Ala Gln Glu Leu Asp Ala Leu Asp Asn Ser His Pro Ile Glu Val			
365	370	375	
agt gtg ggc cat cca tct gag gtt gat gag ata ttt gat gct ata tca			1264
Ser Val Gly His Pro Ser Glu Val Asp Glu Ile Phe Asp Ala Ile Ser			
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Asp Lys Asp Phe Lys Lys Gly Met Asn Met Tyr Leu Thr Lys Phe Gln															
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caa aag aat gct gcc aca gag gat ctc tgg gaa agt tta gaa aat gct	1408														
Gln Lys Asn Ala Ala Thr Glu Asp Leu Trp Glu Ser Leu Glu Asn Ala															
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Ser Gly Lys Pro Ile Ala Ala Val Met Asn Thr Trp Thr Lys Gln Met															
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Glu Asp Pro Asn Gln Ala Lys Leu Lys Ile Leu Met Asp Lys Pro Glu															
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ctg gaa agt tta tta cca ggc att cgt gac ctt tct ctg ccc cct gtg			1792
Leu Glu Ser Leu Leu Pro Gly Ile Arg Asp Leu Ser Leu Pro Pro Val			
555	560	565	
gat cga ctt gga tta cag aat gac ctc ttc tcc ttg gct cga gct gga			1840
Asp Arg Leu Gly Leu Gln Asn Asp Leu Phe Ser Leu Ala Arg Ala Gly			
570	575	580	585
atc att agc act gta gag gtt cta aaa gtc atg gag gct ttt gtg aat			1888
Ile Ile Ser Thr Val Glu Val Leu Lys Val Met Glu Ala Phe Val Asn			
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gag ccc aat tat act gta tgg agc gac ctg agc tgt aac ctg ggg att			1936
Glu Pro Asn Tyr Thr Val Trp Ser Asp Leu Ser Cys Asn Leu Gly Ile			
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ctc tca act ctc ttg tcc cac aca gac ttc tat gag gaa atc cag gag			1984
Leu Ser Thr Leu Leu Ser His Thr Asp Phe Tyr Glu Glu Ile Gln Glu			
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ttt gtg aaa gat gtc ttt tca cct ata ggg gag aga ctg ggc tgg gac			2032
Phe Val Lys Asp Val Phe Ser Pro Ile Gly Glu Arg Leu Gly Trp Asp			
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ccc aaa cct gga gaa ggt cat ctc gat gca ctc ctg agg ggc ttg gtt			2080
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685	690	695		
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act act tta gat att atg tta aaa ctt cat aaa caa gca gat atg caa	2272			
Thr Thr Leu Asp Ile Met Leu Lys Leu His Lys Gln Ala Asp Met Gln				
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gaa gag aaa aac cga atc gaa aga gtc ctt ggc gct act ctt ttg cct	2320			
Glu Glu Lys Asn Arg Ile Glu Arg Val Leu Gly Ala Thr Leu Leu Pro				
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Pro Gln Asp Thr Val Ser Val Ile Gly Gly Val Ala Gly Gly Ser Lys				
765	770	775		
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Leu Ser Val Glu Gly Phe Ala Val Asp Lys Met Ala Gly Glu Val Lys			
810	815	820	825
gct ttc ttc gag agt cac cca gct cct tca gct gag cgt acc atc cag			2608
Ala Phe Phe Glu Ser His Pro Ala Pro Ser Ala Glu Arg Thr Ile Gln			
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Gln Cys Cys Glu Asn Ile Leu Leu Asn Ala Ala Trp Leu Lys Arg Asp			
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gct gag agc atc cac cag tac ctc ctt cag cgg aag gcc tca cca ccc			2704
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Arg Lys Pro Tyr Pro Asp Asp Glu Asn Leu Val Glu Val Lys Phe Ala
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Arg Thr Pro Val Met Ser Thr Tyr Leu Val Ala Phe Val Val Gly Glu
195 200 205

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Ile	Glu	Tyr	Leu	Cys	Val	Asp	His	Cys	Phe	Pro	Glu	Tyr	Asp	Ile	Trp
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Thr	Gln	Phe	Val	Ser	Ala	Asp	Tyr	Thr	Arg	Ala	Gln	Glu	Leu	Asp	Ala
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485 490 495
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Ile Arg Asp Leu Ser Leu Pro Pro Val Asp Arg Leu Gly Leu Gln Asn
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 625 630 635 640
 Pro Ile Gly Glu Arg Leu Gly Trp Asp Pro Lys Pro Gly Glu Gly His
 645 650 655
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 Gly His Lys Ala Thr Leu Glu Glu Ala Arg Arg Arg Phe Lys Asp His
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 Val Glu Gly Lys Gln Ile Leu Ser Ala Asp Leu Arg Ser Pro Val Tyr
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 705 710 715 720
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PH-1064PCT-US seq.TXT

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Val	Asp	Lys	Met	Ala	Gly	Glu	Val	Lys	Ala	Phe	Phe	Glu	Ser	His	Pro
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PH-1064PCT-US seq.TXT

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caa tagaatatgt gatgtgtgaa ttttctttaa aaaacttaag gagtctttgc 1380

Gln

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<210> 13

<211> 1953

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Tyr Ile Asp Arg Val Arg Ser Leu Glu Thr Glu Asn Ala Gly Leu Arg	
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Leu Arg Ile Thr Glu Ser Glu Glu Val Val Ser Arg Glu Val Ser Gly	
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Asp Ser Val Ala Lys Glu Arg Ala Arg Leu Gln Leu Glu Leu Ser Lys	
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Val Arg Glu Glu Phe Lys Glu Leu Lys Ala Arg Asn Thr Lys Lys Glu	
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Glu Ala Ala Leu Gly Glu Ala Lys Lys Gln Leu Gln Asp Glu Met Leu	
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Val Gly Ala Ala His Glu Glu Leu Gln Gln Ser Arg Ile Arg Ile Asp	
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Val Asp Glu Glu Gly Lys Phe Val Arg Leu Arg Asn Lys Ser Asn Glu	
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Pro Leu Leu Thr Tyr Arg Phe Pro Pro Lys Phe Thr Leu Lys Ala Gly	
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Gln Val Val Thr Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro	
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 485 490 495
 Ile Trp Ala Ala Gly Ala Gly Ala Thr His Ser Pro Pro Thr Asp Leu
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 Val Trp Lys Ala Gln Asn Thr Trp Gly Cys Gly Asn Ser Leu Arg Thr
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Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp
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<400> 16

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Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp

35 40 45

Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Phe Glu Lys Lys Arg

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Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro

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Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro		
305	310	315
Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu		
325	330	335
Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr		
340	345	350
Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro		
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Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro		
370	375	380
Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu		
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<213> Homo sapiens

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<222> (164)..(2665)

<400> 17

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Met Lys Tyr Lys

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aat ctt atg gca agg gcc tta tat gac aat gtc cca gag tgt gcc gag 223

Asn Leu Met Ala Arg Ala Leu Tyr Asp Asn Val Pro Glu Cys Ala Glu

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gaa ctg gcc ttt cgc aag gga gac atc ctg acc gtc ata gag cag aac 271

Glu Leu Ala Phe Arg Lys Gly Asp Ile Leu Thr Val Ile Glu Gln Asn

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aca ggg gga ctg gaa gga tgg tgg ctg tgc tcg tta cac ggt cgg caa 319

Thr Gly Gly Leu Glu Gly Trp Trp Leu Cys Ser Leu His Gly Arg Gln

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Gly Ile Val Pro Gly Asn Arg Val Lys Leu Leu Ile Gly Pro Met Gln

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ccc cga gac acc atc tac caa gtg cca cct tcc tac caa aat cag gga 511
Pro Arg Asp Thr Ile Tyr Gln Val Pro Pro Ser Tyr Gln Asn Gln Gly
105          110          115

att tac caa gtc ccc act ggc cac ggc acc caa gaa caa gag gta tat 559
Ile Tyr Gln Val Pro Thr Gly His Gly Thr Gln Glu Gln Glu Val Tyr
120          125          130

cag gtg cca cca tca gtg cag aga agc att ggg gga acc agt ggg ccc 607
Gln Val Pro Pro Ser Val Gln Arg Ser Ile Gly Gly Thr Ser Gly Pro
135          140          145

cac gtg ggt aaa aag gtg ata acc ccc gtg agg aca ggc cat ggc tac 655
His Val Gly Lys Lys Val Ile Thr Pro Val Arg Thr Gly His Gly Tyr
150          155          160

gta tac gag tac cca tcc aga tac caa aag gat gtc tat gat atc cct 703
Val Tyr Glu Tyr Pro Ser Arg Tyr Gln Lys Asp Val Tyr Asp Ile Pro
165          170          175          180

cct tct cat acc act caa ggg gta tac gac atc cct ccc tca tca gca 751
Pro Ser His Thr Thr Gln Gly Val Tyr Asp Ile Pro Pro Ser Ser Ala
185          190          195

aaa ggc cct gtg ttt tca gtt cca gtg gga gag ata aaa cct caa ggg 799
Lys Gly Pro Val Phe Ser Val Pro Val Gly Glu Ile Lys Pro Gln Gly
200          205          210

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Ala Cys Arg Asp Glu Ala Gly Leu Arg Glu Lys Asp Tyr Asp Phe Pro	
230 235 240	
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Pro Pro Met Arg Gln Ala Gly Arg Pro Asp Leu Arg Pro Glu Gly Val	
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Tyr Asp Ile Pro Pro Thr Cys Thr Lys Pro Ala Gly Lys Asp Leu His	
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Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu Pro Val Ala Arg	
280 285 290	
agg cac cag agc ctg tcc ccg aat cac cca ccc ccg caa ctc gga cag	1087
Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro Gln Leu Gly Gln	
295 300 305	
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Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro Arg Gly Val Gln	
310 315 320	
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Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu Ser Phe Ser Ser	
360 365 370	
aca ggc agc acc ccg agt aac atg tcc acg tct tcc acc tcc tcc aag	1327
Thr Gly Ser Thr Arg Ser Asn Met Ser Thr Ser Ser Thr Ser Ser Lys	
375 380 385	
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Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys Arg Leu Phe Leu	
390 395 400	
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Asp Pro Asp Thr Ala Ile Glu Arg Leu Gln Arg Leu Gln Gln Ala Leu	
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Cys Tyr Gly Tyr Met Glu Arg His Ile Asn Glu Ile Arg Thr Ala Val	
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Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His Gln Ile Leu Ser
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Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser Leu Asn Ile Leu
505 510 515
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520 525 530
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Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln Leu Thr Thr Thr
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atc aac acc aac gca gag gcc ctc ttc aga ccc ggc cct ggc agc ttg 1855
Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly Pro Gly Ser Leu
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His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser Thr Glu Tyr Pro
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cac ggt ggc tcc cag gga cag ctg ctg cat cct ggt gac cac aag gcc 1951
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Pro Asp Cys Ser Ser Ser Asp Gly Ser Glu Arg Ser Trp Met Asp Asp	
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tac gat tac gtc cac cta cag ggt aag gag gag ttt gag agg caa cag	2095
Tyr Asp Tyr Val His Leu Gln Gly Lys Glu Glu Phe Glu Arg Gln Gln	
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Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln Asn Lys Met Gln	
645 650 655 660	
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Thr Lys Pro Val Glu Asn Asp Ile Ser Lys Trp Lys Pro Ser Gln Ser	
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Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser Ala His Lys Leu
745 750 755
gtg ttc att gga gac acg ctg aca cgg cag gtg act gcc cag gac att 2479
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760 765 770
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Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys Glu Gln Leu Lys
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act ata gtc atg gca acc aag atg gcc gcc ctc cat tac ccc agc acc 2575
Thr Ile Val Met Ala Thr Lys Met Ala Ala Leu His Tyr Pro Ser Thr
790 795 800
acg gcc ctg cag gaa atg gtg cac caa gtg aca gac ctt tct aga aat 2623
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gcc cag ctg ttc aag cgc tct ttg ctg gag atg gca acg ttc 2665
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His	Gly	Arg	Gln	Gly	Ile	Val	Pro	Gly	Asn	Arg	Val	Lys	Leu	Leu	Ile
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Gly	Pro	Met	Gln	Glu	Thr	Ala	Ser	Ser	His	Glu	Gln	Pro	Ala	Ser	Gly
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Thr	Ser	Gly	Pro	His	Val	Gly	Lys	Lys	Val	Ile	Thr	Pro	Val	Arg	Thr
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 260 265 270
 Lys Asp Leu His Val Lys Tyr Asn Cys Asp Ile Pro Gly Ala Ala Glu
 275 280 285
 Pro Val Ala Arg Arg His Gln Ser Leu Ser Pro Asn His Pro Pro Pro
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 Gln Leu Gly Gln Ser Val Gly Ser Gln Asn Asp Ala Tyr Asp Val Pro
 305 310 315 320
 Arg Gly Val Gln Phe Leu Glu Pro Pro Ala Glu Thr Ser Glu Lys Ala
 325 330 335
 Asn Pro Gln Glu Arg Asp Gly Val Tyr Asp Val Pro Leu His Asn Pro
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 Pro Asp Ala Lys Gly Ser Arg Asp Leu Val Asp Gly Ile Asn Arg Leu
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 Thr Ser Ser Lys Glu Ser Ser Leu Ser Ala Ser Pro Ala Gln Asp Lys
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Arg Thr Ala Val Asp Lys Val Glu Leu Phe Leu Lys Glu Tyr Leu His			
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Leu His Asn Lys Met Lys Arg Glu Leu Gln Arg Val Glu Asp Ser His			
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Gln Ile Leu Ser Gln Thr Ser His Asp Leu Asn Glu Cys Ser Trp Ser			
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Leu Asn Ile Leu Ala Ile Asn Lys Pro Gln Asn Lys Cys Asp Asp Leu			
515	520	525	
Asp Arg Phe Val Met Val Ala Lys Thr Val Pro Asp Asp Ala Lys Gln			
530	535	540	
Leu Thr Thr Thr Ile Asn Thr Asn Ala Glu Ala Leu Phe Arg Pro Gly			
545	550	555	560
Pro Gly Ser Leu His Leu Lys Asn Gly Pro Glu Ser Ile Met Asn Ser			
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 Glu Arg Gln Gln Lys Glu Leu Leu Glu Lys Glu Asn Ile Met Lys Gln
 645 650 655
 Asn Lys Met Gln Leu Glu His His Gln Leu Ser Gln Phe Gln Leu Leu
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 675 680 685
 Pro Ser Gln Ser Leu Pro Thr Thr Asn Ser Gly Val Ser Ala Gln Asp
 690 695 700
 Arg Gln Leu Leu Cys Phe Tyr Tyr Asp Gln Cys Glu Thr His Phe Ile
 705 710 715 720
 Ser Leu Leu Asn Ala Ile Asp Ala Leu Phe Ser Cys Val Ser Ser Ala
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 Gln Pro Pro Arg Ile Phe Val Ala His Ser Lys Phe Val Ile Leu Ser
 740 745 750
 Ala His Lys Leu Val Phe Ile Gly Asp Thr Leu Thr Arg Gln Val Thr
 755 760 765
 Ala Gln Asp Ile Arg Asn Lys Val Met Asn Ser Ser Asn Gln Leu Cys
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Tyr Pro Ser Thr Thr Ala Leu Gln Glu Met Val His Gln Val Thr Asp
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<212> DNA

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Gln Gly Leu Gly Pro Gly Ser Thr Val Leu Leu Val Val Asp Lys Cys			
55	60	65	70
gac gaa cct ctg agc atc ctg gtg agg aat aac aag ggc cgc agc agc 293			
Asp Glu Pro Leu Ser Ile Leu Val Arg Asn Asn Lys Gly Arg Ser Ser			
	75	80	85
acc tac gag gtg cgg ctg acg cag acc gtg gcc cac ctg aag cag caa 341			
Thr Tyr Glu Val Arg Leu Thr Gln Thr Val Ala His Leu Lys Gln Gln			
90	95	100	
gtg agc ggg ctg gag ggt gtg cag gac gac ctg ttc tgg ctg acc ttc 389			
Val Ser Gly Leu Glu Gly Val Gln Asp Asp Leu Phe Trp Leu Thr Phe			
105	110	115	
gag ggg aag ccc ctg gag gac cag ctc ccg ctg ggg gag tac ggc ctc 437			
Glu Gly Lys Pro Leu Glu Asp Gln Leu Pro Leu Gly Glu Tyr Gly Leu			
120	125	130	
aag ccc ctg agc acc gtg ttc atg aat ctg cgc ctg cgg gga ggc ggc 485			
Lys Pro Leu Ser Thr Val Phe Met Asn Leu Arg Leu Arg Gly Gly Gly			
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155

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25

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His Cys Phe Ser Ser Ser Pro Asn Glu Trp Leu Gln Ser Val Gln Ala

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75

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ttc tgc caa ctc ttc acc ctc acc aag ggg ggc agg ttt tac atc act 346

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90

95

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atc tac acg gtg agg cac ccg gag tgg cat ctc acc tcg gat tac tcc 442

Ile Tyr Thr Val Arg His Pro Glu Trp His Leu Thr Ser Asp Tyr Ser

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tac ggt ttc gcc tac atc ctg gcc tgg gtg gcc ttc ccc ctg gcc ctt 490

Tyr Gly Phe Ala Tyr Ile Leu Ala Trp Val Ala Phe Pro Leu Ala Leu

135 140 145

ctc agc ggt gtc atc tat gtg atc ttg cgg aaa cgc gaa tgaggcgccc 539

Leu Ser Gly Val Ile Tyr Val Ile Leu Arg Lys Arg Glu

150 155 160

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<211> 160

<212> PRT

<213> Homo sapiens

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Asn	Val	His	His	Cys	Phe	Ser	Ser	Ser	Pro	Asn	Glu	Trp	Leu	Gln	Ser
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Val	Gln	Ala	Thr	Met	Ile	Leu	Ser	Ile	Ile	Phe	Ser	Ile	Leu	Ser	Leu
				65				70				75			80
Phe	Leu	Phe	Phe	Cys	Gln	Leu	Phe	Thr	Leu	Thr	Lys	Gly	Gly	Arg	Phe
				85								90			95
Tyr	Ile	Thr	Gly	Ile	Phe	Gln	Ile	Leu	Ala	Gly	Leu	Cys	Val	Met	Ser

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<222> (36)..(2717)

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Arg Met Gly Arg Val Pro Leu Ala Trp Cys Leu Ala Leu Cys Gly Trp	
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gcg tgc atg gcc ccc agg ggc acg cag gct gaa gaa agt ccc ttc gtg	149
Ala Cys Met Ala Pro Arg Gly Thr Gln Ala Glu Glu Ser Pro Phe Val	

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Arg Cys Gln Leu Gln Val Gln Gly Glu Pro Pro Glu Val His Trp Leu			
55	60	65	70
cgg gat gga cag atc ctg gag ctc gcg gac agc acc cag acc cag gtg	293		
Arg Asp Gly Gln Ile Leu Glu Leu Ala Asp Ser Thr Gln Thr Gln Val			
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ccc ctg ggt gag gat gaa cag gat gac tgg ata gtg gtc agc cag ctc	341		
Pro Leu Gly Glu Asp Glu Gln Asp Asp Trp Ile Val Val Ser Gln Leu			
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aga atc acc tcc ctg cag ctt tcc gac acg gga cag tac cag tgt ttg	389		
Arg Ile Thr Ser Leu Gln Leu Ser Asp Thr Gly Gln Tyr Gln Cys Leu			
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gtg ttt ctg gga cat cag acc ttc gtg tcc cag cct ggc tat gtt ggg	437		
Val Phe Leu Gly His Gln Thr Phe Val Ser Gln Pro Gly Tyr Val Gly			
120	125	130	
ctg gag ggc ttg cct tac ttc ctg gag gag ccc gaa gac agg act gtg	485		
Leu Glu Gly Leu Pro Tyr Phe Leu Glu Glu Pro Glu Asp Arg Thr Val			
135	140	145	150
gcc gcc aac acc ccc ttc aac ctg agc tgc caa gct cag gga ccc cca	533		
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Glu Pro Val Asp Leu Leu Trp Leu Gln Asp Ala Val Pro Leu Ala Thr			
170	175	180	
gct cca ggt cac ggc ccc cag cgc agc ctg cat gtt cca ggg ctg aac			629
Ala Pro Gly His Gly Pro Gln Arg Ser Leu His Val Pro Gly Leu Asn			
185	190	195	
aag aca tcc tct ttc tcc tgc gaa gcc cat aac gcc aag ggg gtc acc			677
Lys Thr Ser Ser Phe Ser Cys Glu Ala His Asn Ala Lys Gly Val Thr			
200	205	210	
aca tcc cgc aca gcc acc atc aca gtg ctc ccc cag cag ccc cgt aac			725
Thr Ser Arg Thr Ala Thr Ile Thr Val Leu Pro Gln Gln Pro Arg Asn			
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ctc cac ctg gtc tcc cgc caa ccc acg gag ctg gag gtg gct tgg act			773
Leu His Leu Val Ser Arg Gln Pro Thr Glu Leu Glu Val Ala Trp Thr			
235	240	245	
cca ggc ctg agc ggc atc tac ccc ctg acc cac tgc acc ctg cag gct			821
Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr His Cys Thr Leu Gln Ala			
250	255	260	
gtg ctg tca gac gat ggg atg ggc atc cag gcg gga gaa cca gac ccc			869
Val Leu Ser Asp Asp Gly Met Gly Ile Gln Ala Gly Glu Pro Asp Pro			
265	270	275	
cca gag gag ccc ctc acc tcg caa gca tcc gtg ccc ccc cat cag ctt			917
Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser Val Pro Pro His Gln Leu			

PH-1064PCT-US seq.TXT

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Arg Leu Gly Ser Leu His Pro His Pro Pro Tyr His Ile Arg Val Ala			
295	300	305	310
tgc acc agc agc cag ggc ccc tca tcc tgg acc cac tgg ctt cct gtg			1013
Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp Thr His Trp Leu Pro Val			
	315	320	325
gag acg ccg gag gga gtg ccc ctg ggc ccc cct gag aac att agt gct			1061
Glu Thr Pro Glu Gly Val Pro Leu Gly Pro Pro Glu Asn Ile Ser Ala			
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Thr Arg Asn Gly Ser Gln Ala Phe Val His Trp Gln Glu Pro Arg Ala			
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ccc ctg cag ggt acc ctg tta ggg tac cgg ctg gcg tat caa ggc cag			1157
Pro Leu Gln Gly Thr Leu Leu Gly Tyr Arg Leu Ala Tyr Gln Gly Gln			
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gac acc cca gag gtg cta atg gac ata ggg cta agg caa gag gtg acc			1205
Asp Thr Pro Glu Val Leu Met Asp Ile Gly Leu Arg Gln Glu Val Thr			
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ctg gag ctg cag ggg gac ggg tct gtg tcc aat ctg aca gtg tgt gtg			1253
Leu Glu Leu Gln Gly Asp Gly Ser Val Ser Asn Leu Thr Val Cys Val			
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Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro Trp Ser Leu Pro Val Pro			

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aag gaa cct tca act cct gcc ttc tcg tgg ccc tgg tgg tat gta ctg			1397
Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp Pro Trp Trp Tyr Val Leu			
440	445	450	
cta gga gca gtc gtg gcc gct gcc tgt gtc ctc atc ttg gct ctc ttc			1445
Leu Gly Ala Val Val Ala Ala Ala Cys Val Leu Ile Leu Ala Leu Phe			
455	460	465	470
ctt gtc cac cgg cga aag aag gag acc cgt tat gga gaa gtg ttt gaa			1493
Leu Val His Arg Arg Lys Lys Glu Thr Arg Tyr Gly Glu Val Phe Glu			
475	480	485	
cca aca gtg gaa aga ggt gaa ctg gta gtc agg tac cgc gtg cgc aag			1541
Pro Thr Val Glu Arg Gly Glu Leu Val Val Arg Tyr Arg Val Arg Lys			
490	495	500	
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Ser Tyr Ser Arg Arg Thr Thr Glu Ala Thr Leu Asn Ser Leu Gly Ile			
505	510	515	
agt gaa gag ctg aag gag aag ctg cgg gat gtg atg gtg gac cgg cac			1637
Ser Glu Glu Leu Lys Glu Lys Leu Arg Asp Val Met Val Asp Arg His			
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aag acg atg aag att gcc atc tgc acg agg tca gag ctg gag gat ttc				1781
Lys Thr Met Lys Ile Ala Ile Cys Thr Arg Ser Glu Leu Glu Asp Phe				
	570	575	580	
ctg agt gaa gcg gtc tgc atg aag gaa ttt gac cat ccc aac gtc atg				1829
Leu Ser Glu Ala Val Cys Met Lys Glu Phe Asp His Pro Asn Val Met				
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agg ctc atc ggt gtc tgt ttc cag ggt tct gaa cga gag agc ttc cca				1877
Arg Leu Ile Gly Val Cys Phe Gln Gly Ser Glu Arg Glu Ser Phe Pro				
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gca cct gtg gtc atc tta cct ttc atg aaa cat gga gac cta cac agc				1925
Ala Pro Val Val Ile Leu Pro Phe Met Lys His Gly Asp Leu His Ser				
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ttc ctc ctc tat tcc cgg ctc ggg ggc cag cca gtg tac ctg ccc act				1973
Phe Leu Leu Tyr Ser Arg Leu Gly Gly Gln Pro Val Tyr Leu Pro Thr				
	635	640	645	
cag atg cta gtg aag ttc atg gca gac atc gcc agt ggc atg gag tat				2021
Gln Met Leu Val Lys Phe Met Ala Asp Ile Ala Ser Gly Met Glu Tyr				
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ctg agt acc aag aga ttc ata cac cgg gac ctg gcg gcc agg aac tgc				2069
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Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg Gln Gly Arg Ile Ala Lys			
695	700	705	710
atg cca gtc aag tgg att gcc att gag agt cta gct gac cgt gtc tac	2213		
Met Pro Val Lys Trp Ile Ala Ile Glu Ser Leu Ala Asp Arg Val Tyr			
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Thr Ser Lys Ser Asp Val Trp Ser Phe Gly Val Thr Met Trp Glu Ile			
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Ala Thr Arg Gly Gln Thr Pro Tyr Pro Gly Val Glu Asn Ser Glu Ile			
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tat gac tat ctg cgc cag gga aat cgc ctg aag cag cct gcg gac tgt	2357		
Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu Lys Gln Pro Ala Asp Cys			
	760	765	770
ctg gat gga ctg tat gcc ttg atg tcg cgg tgc tgg gag cta aat ccc	2405		
Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg Cys Trp Glu Leu Asn Pro			
775	780	785	790
cag gac cgg cca agt ttt aca gag ctg cgg gaa gat ttg gag aac aca	2453		
Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg Glu Asp Leu Glu Asn Thr			

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795

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805

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815

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Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu Pro Pro Gly Ala Ala Gly

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865

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885

gcc cca ggg cag gag gat ggt gcc tgagacaacc ctccacctgg tactccctct 2747

Ala Pro Gly Gln Glu Asp Gly Ala

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<212> PRT

<213> Homo sapiens

<400> 26

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Gly	Leu	Thr	Gly	Thr	Leu	Arg	Cys	Gln	Leu	Gln	Val	Gln	Gly	Glu	Pro
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Ile	Val	Val	Ser	Gln	Leu	Arg	Ile	Thr	Ser	Leu	Gln	Leu	Ser	Asp	Thr
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Leu Glu Val Ala Trp Thr Pro Gly Leu Ser Gly Ile Tyr Pro Leu Thr		
245	250	255
His Cys Thr Leu Gln Ala Val Leu Ser Asp Asp Gly Met Gly Ile Gln		
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Ala Gly Glu Pro Asp Pro Pro Glu Glu Pro Leu Thr Ser Gln Ala Ser		
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Val Pro Pro His Gln Leu Arg Leu Gly Ser Leu His Pro His Pro Pro		
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Tyr His Ile Arg Val Ala Cys Thr Ser Ser Gln Gly Pro Ser Ser Trp		
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Thr His Trp Leu Pro Val Glu Thr Pro Glu Gly Val Pro Leu Gly Pro		

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355	360	365
Leu Ala Tyr Gln Gly Gln Asp Thr Pro Glu Val Leu Met Asp Ile Gly		
370	375	380
Leu Arg Gln Glu Val Thr Leu Glu Leu Gln Gly Asp Gly Ser Val Ser		
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Asn Leu Thr Val Cys Val Ala Ala Tyr Thr Ala Ala Gly Asp Gly Pro		
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Trp Ser Leu Pro Val Pro Leu Glu Ala Trp Arg Pro Gly Glu Ala Gln		
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Pro Val His Gln Leu Val Lys Glu Pro Ser Thr Pro Ala Phe Ser Trp		
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Leu Ile Leu Ala Leu Phe Leu Val His Arg Arg Lys Lys Glu Thr Arg		
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Ile Leu Lys Val Ala Val Lys Thr Met Lys Ile Ala Ile Cys Thr Arg		
565	570	575
Ser Glu Leu Glu Asp Phe Leu Ser Glu Ala Val Cys Met Lys Glu Phe		
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Glu Arg Glu Ser Phe Pro Ala Pro Val Val Ile Leu Pro Phe Met Lys		
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Pro Val Tyr Leu Pro Thr Gln Met Leu Val Lys Phe Met Ala Asp Ile		
645	650	655
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Leu Ala Ala Arg Asn Cys Met Leu Asn Glu Asn Met Ser Val Cys Val		
675	680	685
Ala Asp Phe Gly Leu Ser Lys Lys Ile Tyr Asn Gly Asp Tyr Tyr Arg		
690	695	700
Gln Gly Arg Ile Ala Lys Met Pro Val Lys Trp Ile Ala Ile Glu Ser		

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Val Glu Asn Ser Glu Ile Tyr Asp Tyr Leu Arg Gln Gly Asn Arg Leu			
755	760	765	
Lys Gln Pro Ala Asp Cys Leu Asp Gly Leu Tyr Ala Leu Met Ser Arg			
770	775	780	
Cys Trp Glu Leu Asn Pro Gln Asp Arg Pro Ser Phe Thr Glu Leu Arg			
785	790	795	800
Glu Asp Leu Glu Asn Thr Leu Lys Ala Leu Pro Pro Ala Gln Glu Pro			
805	810	815	
Asp Glu Ile Leu Tyr Val Asn Met Asp Glu Gly Gly Gly Tyr Pro Glu			
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Pro Pro Gly Ala Ala Gly Gly Ala Asp Pro Pro Thr Gln Pro Asp Pro			
835	840	845	
Lys Asp Ser Cys Ser Cys Leu Thr Ala Ala Glu Val His Pro Ala Gly			
850	855	860	
Arg Tyr Val Leu Cys Pro Ser Thr Thr Pro Ser Pro Ala Gln Pro Ala			
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<211> 3781

<212> DNA

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<222> (4)..(2994)

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                20                25                30
ctt aag gag aga tgg ggc tcc aac gag tta ccg gct gaa gaa gga aaa     144
Leu Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys
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acc ttg ctg gaa ctt gtg att gag cag ttt gaa gac ttg cta gtt agg     192
Thr Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg
                50                55                60
att tta tta ctg gca gca tgt ata tct ttt gtt ttg gct tgg ttt gaa     240
Ile Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu
                65                70                75
gaa ggt gaa gaa aca att aca gcc ttt gta gaa cct ttt gta att tta     288

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Glu Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu

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PH-1064PCT-US seq.TXT

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Leu Phe Ser Gly Thr Asn Ile Ala Ala Gly Lys Ala Met Gly Val Val
      210              215              220
gta gca act gga gtt aac acc gaa att ggc aag atc cgg gat gaa atg 720
Val Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met
      225              230              235
gtg gca aca gaa cag gag aga aca ccc ctt cag caa aaa cta gat gaa 768
Val Ala Thr Glu Gln Glu Arg Thr Pro Leu Gln Gln Lys Leu Asp Glu
240              245              250              255
ttt ggg gaa cag ctt tcc aaa gtc atc tcc ctt att tgc att gca gtc 816
Phe Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val
      260              265              270
tgg atc ata aat att ggg cac ttc aat gac ccg gtt cat gga ggg tcc 864
Trp Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser
      275              280              285
tgg atc aga ggt gct att tac tac ttt aaa att gca gtg gcc ctg gct 912
Trp Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala
      290              295              300
gta gca gcc att cct gaa ggt ctg cct gca gtc atc acc acc tgc ctg 960
Val Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu
      305              310              315
gct ctt gga act cgc aga atg gca aag aaa aat gcc att gtt cga agc 1008
Ala Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser
      320              325              330              335
ctc ccg tct gtg gaa acc ctt ggt tgt act tct gtt atc tgc tca gac 1056

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Leu Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp

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PH-1064PCT-US seq.TXT

Lys Ile Glu Arg Ala Asn Ala Cys Asn Ser Val Ile Lys Gln Leu Met
465 470 475
aaa aag gaa ttc act cta gag ttt tca cgt gac aga aag tca atg tcg 1488
Lys Lys Glu Phe Thr Leu Glu Phe Ser Arg Asp Arg Lys Ser Met Ser
480 485 490 495
gtt tac tgt aca cca aat aaa cca agc agg aca tca atg agc aag atg 1536
Val Tyr Cys Thr Pro Asn Lys Pro Ser Arg Thr Ser Met Ser Lys Met
500 505 510
ttt gtg aag ggt gct cct gaa ggt gtc att gac agg tgc acc cac att 1584
Phe Val Lys Gly Ala Pro Glu Gly Val Ile Asp Arg Cys Thr His Ile
515 520 525
cga gtt gga agt act aag gtt cct atg acc tct gga gtc aaa cag aag 1632
Arg Val Gly Ser Thr Lys Val Pro Met Thr Ser Gly Val Lys Gln Lys
530 535 540
atc atg tct gtc att cga gag tgg ggt agt ggc agc gac aca ctg cga 1680
Ile Met Ser Val Ile Arg Glu Trp Gly Ser Gly Ser Asp Thr Leu Arg
545 550 555
tgc ctg gcc ctg gcc act cat gac aac cca ctg aga aga gaa gaa atg 1728
Cys Leu Ala Leu Ala Thr His Asp Asn Pro Leu Arg Arg Glu Glu Met
560 565 570 575
cac ctt gag gac tct gcc aac ttt att aaa tat gag acc aat ctg acc 1776
His Leu Glu Asp Ser Ala Asn Phe Ile Lys Tyr Glu Thr Asn Leu Thr
580 585 590
ttc gtt ggc tgc gtg ggc atg ctg gat cct ccg aga atc gag gtg gcc 1824

PH-1064PCT-US seq.TXT

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tcc tcc gtg aag ctg tgc cgg caa gca ggc atc cgg gtc atc atg atc	1872
Ser Ser Val Lys Leu Cys Arg Gln Ala Gly Ile Arg Val Ile Met Ile	
610	615
620	
act ggg gac aac aag ggc act gct gtg gcc atc tgt cgc cgc atc ggc	1920
Thr Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly	
625	630
635	
atc ttc ggg cag gat gag gac gtg acg tca aaa gct ttc aca ggc cgg	1968
Ile Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg	
640	645
650	655
gag ttt gat gaa ctc aac ccc tcc gcc cag cga gac gcc tgc ctg aac	2016
Glu Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn	
660	665
670	
gcc cgc tgt ttt gct cga gtt gaa ccc tcc cac aag tct aaa atc gta	2064
Ala Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val	
675	680
685	
gaa ttt ctt cag tct ttt gat gag att aca gct atg act ggc gat ggc	2112
Glu Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly	
690	695
700	
gtg aac gat gct cct gct ctg aag aaa gcc gag att ggc att gct atg	2160
Val Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met	
705	710
715	
ggc tct ggc act gcg gtg gct aaa acc gcc tct gag atg gtc ctg gcg	2208

PH-1064PCT-US seq.TXT

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Asp	Asp	Asn	Phe	Ser	Thr	Ile	Val	Ala	Ala	Val	Glu	Glu	Gly	Arg	Ala	
				740						745					750	
atc	tac	aac	aac	atg	aaa	cag	ttc	atc	cgc	tac	ctc	atc	tcg	tcc	aac	2304
Ile	Tyr	Asn	Asn	Met	Lys	Gln	Phe	Ile	Arg	Tyr	Leu	Ile	Ser	Ser	Asn	
				755						760					765	
gtc	ggg	gaa	gtt	gtc	tgt	att	ttc	ctg	aca	gca	gcc	ctt	gga	ttt	ccc	2352
Val	Gly	Glu	Val	Val	Cys	Ile	Phe	Leu	Thr	Ala	Ala	Leu	Gly	Phe	Pro	
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gag	gct	ttg	att	cct	gtt	cag	ctg	ctc	tgg	gtc	aat	ctg	gtg	aca	gat	2400
Glu	Ala	Leu	Ile	Pro	Val	Gln	Leu	Leu	Trp	Val	Asn	Leu	Val	Thr	Asp	
				785						790					795	
ggc	ctg	cct	gcc	act	gca	ctg	ggg	ttc	aac	cct	cct	gat	ctg	gac	atc	2448
Gly	Leu	Pro	Ala	Thr	Ala	Leu	Gly	Phe	Asn	Pro	Pro	Asp	Leu	Asp	Ile	
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atg	aat	aaa	cct	ccc	cgg	aac	cca	aag	gaa	cca	ttg	atc	agc	ggg	tgg	2496
Met	Asn	Lys	Pro	Pro	Arg	Asn	Pro	Lys	Glu	Pro	Leu	Ile	Ser	Gly	Trp	
					820					825					830	
ctc	ttt	ttc	cgt	tac	ttg	gct	att	ggc	tgt	tac	gtc	ggc	gct	gct	acc	2544
Leu	Phe	Phe	Arg	Tyr	Leu	Ala	Ile	Gly	Cys	Tyr	Val	Gly	Ala	Ala	Thr	
					835					840					845	
gtg	ggt	gct	gct	gca	tgg	tgg	ttc	att	gct	gct	gac	ggt	ggt	cca	aga	2592

PH-1064PCT-US seq.TXT

Val Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg	
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Val Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn	
865	870
875	
ccg gac ttt gaa ggc gtg gat tgt gca atc ttt gaa tcc cca tac ccg	2688
Pro Asp Phe Glu Gly Val Asp Cys Ala Ile Phe Glu Ser Pro Tyr Pro	
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890	895
atg aca atg gcg ctc tct gtt cta gta act ata gaa atg tgt aac gcc	2736
Met Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala	
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ctc aac agc ttg tcc gaa aac cag tcc ttg ctg agg atg ccc ccc tgg	2784
Leu Asn Ser Leu Ser Glu Asn Gln Ser Leu Leu Arg Met Pro Pro Trp	
915	920
925	
gag aac atc tgg ctc gtg ggc tcc atc tgc ctg tcc atg tca ctc cac	2832
Glu Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His	
930	935
940	
ttc ctg atc ctc tat gtc gaa ccc ttg cca ctc atc ttc cag atc aca	2880
Phe Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr	
945	950
955	
ccg ctg aac gtg acc cag tgg ctg atg gtg ctg aaa atc tcc ttg ccc	2928
Pro Leu Asn Val Thr Gln Trp Leu Met Val Leu Lys Ile Ser Leu Pro	
960	965
970	975
gtg att ctc atg gat gag acg ctc aag ttt gtg gcc cgc aac tac ctg	2976

PH-1064PCT-US seq.TXT

Val Ile Leu Met Asp Glu Thr Leu Lys Phe Val Ala Arg Asn Tyr Leu

980

985

990

gaa cct gca ata ctg gag taaccgcttc ctaaaccatt ttgcagaaat 3024

Glu Pro Ala Ile Leu Glu

995

gtaagggtgt tcggttgctg gcatgtgcgt ttttagcaac acatctacca accctgtgca 3084

tgactgatgt tggggaaaaa gaaaagtaaa aaacttccca actcactttg tgttatgtgg 3144

aggaaatgtg tattaccaat ggggttgcta gcttttaaata caaaatactg attacagatg 3204

tacaatttag cttaatcaga aagcctctcc agagaagttt ggtttctttg ctgcaagagg 3264

aatgaggctc tgtaacctta tctaagaact tggaagccgt cagccaagtc gccacatttc 3324

tctgcaaaat gtcatagctt atataaatgt acagtattca attgtaatgc atgcttcggt 3384

tgtaagtagc cagatccctc tccagtgaca ttggaacatg ctacttttta attggccctg 3444

tacagtttgc ttatttataa attcattaaa aacactacag gtggttgatg gttaaaatgt 3504

aggcctccag ttcattttca gttattttct gagtgtgcag acagctatct cgcactgtat 3564

taaatgtaac ttatttaatg aaatcagaag cagtagacag atgttggtgc aatacaaata 3624

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<210> 28

<211> 997

<212> PRT

<213> Homo sapiens

<400> 28

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PH-1064PCT-US seq.TXT

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Lys Glu Arg Trp Gly Ser Asn Glu Leu Pro Ala Glu Glu Gly Lys Thr			
35	40	45	
Leu Leu Glu Leu Val Ile Glu Gln Phe Glu Asp Leu Leu Val Arg Ile			
50	55	60	
Leu Leu Leu Ala Ala Cys Ile Ser Phe Val Leu Ala Trp Phe Glu Glu			
65	70	75	80
Gly Glu Glu Thr Ile Thr Ala Phe Val Glu Pro Phe Val Ile Leu Leu			
85	90	95	
Ile Leu Val Ala Asn Ala Ile Val Gly Val Trp Gln Glu Arg Asn Ala			
100	105	110	
Glu Asn Ala Ile Glu Ala Leu Lys Glu Tyr Glu Pro Glu Met Gly Lys			
115	120	125	
Val Tyr Arg Gln Asp Arg Lys Ser Val Gln Arg Ile Lys Ala Lys Asp			
130	135	140	
Ile Val Pro Gly Asp Ile Val Glu Ile Ala Val Gly Asp Lys Val Pro			
145	150	155	160
Ala Asp Ile Arg Leu Thr Ser Ile Lys Ser Thr Thr Leu Arg Val Asp			
165	170	175	
Gln Ser Ile Leu Thr Gly Glu Ser Val Ser Val Ile Lys His Thr Asp			
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Pro Val Pro Asp Pro Arg Ala Val Asn Gln Asp Lys Lys Asn Met Leu			

PH-1064PCT-US seq.TXT

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Ala Thr Gly Val Asn Thr Glu Ile Gly Lys Ile Arg Asp Glu Met Val		
225	230	235
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245	250	255
Gly Glu Gln Leu Ser Lys Val Ile Ser Leu Ile Cys Ile Ala Val Trp		
260	265	270
Ile Ile Asn Ile Gly His Phe Asn Asp Pro Val His Gly Gly Ser Trp		
275	280	285
Ile Arg Gly Ala Ile Tyr Tyr Phe Lys Ile Ala Val Ala Leu Ala Val		
290	295	300
Ala Ala Ile Pro Glu Gly Leu Pro Ala Val Ile Thr Thr Cys Leu Ala		
305	310	315
Leu Gly Thr Arg Arg Met Ala Lys Lys Asn Ala Ile Val Arg Ser Leu		
325	330	335
Pro Ser Val Glu Thr Leu Gly Cys Thr Ser Val Ile Cys Ser Asp Lys		
340	345	350
Thr Gly Thr Leu Thr Thr Asn Gln Met Ser Val Cys Arg Met Phe Ile		
355	360	365
Leu Asp Arg Val Glu Gly Asp Thr Cys Ser Leu Asn Glu Phe Thr Ile		
370	375	380
Thr Gly Ser Thr Tyr Ala Pro Ile Gly Glu Val His Lys Asp Asp Lys		

PH-1064PCT-US seq.TXT

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Pro	Val	Asn	Cys	His	Gln	Tyr	Asp	Gly	Leu	Val	Glu	Leu	Ala	Thr	Ile
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Cys	Ala	Leu	Cys	Asn	Asp	Ser	Ala	Leu	Asp	Tyr	Asn	Glu	Ala	Lys	Gly
		420						425					430		
Val	Tyr	Glu	Lys	Val	Gly	Glu	Ala	Thr	Glu	Thr	Ala	Leu	Thr	Cys	Leu
		435						440					445		
Val	Glu	Lys	Met	Asn	Val	Phe	Asp	Thr	Glu	Leu	Lys	Gly	Leu	Ser	Lys
		450						455					460		
Ile	Glu	Arg	Ala	Asn	Ala	Cys	Asn	Ser	Val	Ile	Lys	Gln	Leu	Met	Lys
465						470							475		480
Lys	Glu	Phe	Thr	Leu	Glu	Phe	Ser	Arg	Asp	Arg	Lys	Ser	Met	Ser	Val
				485						490				495	
Tyr	Cys	Thr	Pro	Asn	Lys	Pro	Ser	Arg	Thr	Ser	Met	Ser	Lys	Met	Phe
			500							505				510	
Val	Lys	Gly	Ala	Pro	Glu	Gly	Val	Ile	Asp	Arg	Cys	Thr	His	Ile	Arg
		515								520				525	
Val	Gly	Ser	Thr	Lys	Val	Pro	Met	Thr	Ser	Gly	Val	Lys	Gln	Lys	Ile
		530								535				540	
Met	Ser	Val	Ile	Arg	Glu	Trp	Gly	Ser	Gly	Ser	Asp	Thr	Leu	Arg	Cys
545						550					555				560
Leu	Ala	Leu	Ala	Thr	His	Asp	Asn	Pro	Leu	Arg	Arg	Glu	Glu	Met	His
				565						570				575	
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PH-1064PCT-US seq.TXT

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610	615	620
Gly Asp Asn Lys Gly Thr Ala Val Ala Ile Cys Arg Arg Ile Gly Ile		
625	630	635
Phe Gly Gln Asp Glu Asp Val Thr Ser Lys Ala Phe Thr Gly Arg Glu		
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Phe Asp Glu Leu Asn Pro Ser Ala Gln Arg Asp Ala Cys Leu Asn Ala		
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Arg Cys Phe Ala Arg Val Glu Pro Ser His Lys Ser Lys Ile Val Glu		
675	680	685
Phe Leu Gln Ser Phe Asp Glu Ile Thr Ala Met Thr Gly Asp Gly Val		
690	695	700
Asn Asp Ala Pro Ala Leu Lys Lys Ala Glu Ile Gly Ile Ala Met Gly		
705	710	715
Ser Gly Thr Ala Val Ala Lys Thr Ala Ser Glu Met Val Leu Ala Asp		
725	730	735
Asp Asn Phe Ser Thr Ile Val Ala Ala Val Glu Glu Gly Arg Ala Ile		
740	745	750
Tyr Asn Asn Met Lys Gln Phe Ile Arg Tyr Leu Ile Ser Ser Asn Val		
755	760	765
Gly Glu Val Val Cys Ile Phe Leu Thr Ala Ala Leu Gly Phe Pro Glu		

PH-1064PCT-US seq.TXT

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	805	810
Asn Lys Pro Pro Arg Asn Pro Lys Glu Pro Leu Ile Ser Gly Trp Leu		815
	820	825
Phe Phe Arg Tyr Leu Ala Ile Gly Cys Tyr Val Gly Ala Ala Thr Val		830
	835	840
Gly Ala Ala Ala Trp Trp Phe Ile Ala Ala Asp Gly Gly Pro Arg Val		845
	850	855
Ser Phe Tyr Gln Leu Ser His Phe Leu Gln Cys Lys Glu Asp Asn Pro		860
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	885	890
Thr Met Ala Leu Ser Val Leu Val Thr Ile Glu Met Cys Asn Ala Leu		895
	900	905
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	915	920
Asn Ile Trp Leu Val Gly Ser Ile Cys Leu Ser Met Ser Leu His Phe		925
	930	935
Leu Ile Leu Tyr Val Glu Pro Leu Pro Leu Ile Phe Gln Ile Thr Pro		940
945	950	955
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PH-1064PCT-US seq.TXT

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<210> 29

<211> 1103

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<213> Homo sapiens

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Met Gly Lys Trp His Val Gly Gly Arg Arg Gly Ser Pro

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10

cgc caa tgg gga gct acg gcg cgc ggc cgg gac ttg gag gcg gtg cgg 219
 Arg Gln Trp Gly Ala Thr Ala Arg Gly Arg Asp Leu Glu Ala Val Arg

15

20

25

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 Arg Gly Gly Cys Gly Ser Val Gly Arg Arg Arg Gln Arg Arg Arg Arg

PH-1064PCT-US seq.TXT

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cgg ccg ggc gac tgc gaa gtt tgt att tct tat ctg gga aga ttt tac	411			
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95	100	105		
aac gaa ctt ata aag ttc tgc cgg gaa gca aga ggc aaa gag aat cgg	507			
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Leu Cys Tyr Tyr Ile Gly Ala Thr Asp Asp Ala Ala Thr Lys Ile Ile				
130	135	140		
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Asn Glu Val Ser Lys Pro Leu Ala His His Ile Pro Val Glu Lys Ile				
145	150	155		
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Cys Glu Lys Leu Lys Lys Lys Asp Ser Gln Ile Cys Glu Leu Lys Tyr				

PH-1064PCT-US seq.TXT

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Lys Glu Leu Lys Lys Ile Leu Asp Asp Trp Gly Glu Thr Cys Lys Gly
190                               195                               200                               205
tgt gca gaa aag tct gac tac atc cgg aag ata aat gaa ctg atg cct 795
Cys Ala Glu Lys Ser Asp Tyr Ile Arg Lys Ile Asn Glu Leu Met Pro
210                               215                               220
aaa tat gcc ccc aag gca gcc agt gca ccg acc gat ttg tagtctgctc 844
Lys Tyr Ala Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu
225                               230
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tttgtaattt attttttaag tgggctcctg acaatactgt atcagatgtg aagcctggag 964
ctttcctgat gatgctggcc ctacagtacc cccatgaggg gattcccttc cttctgttgc 1024
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<210> 30

<211> 234

<212> PRT

<213> Homo sapiens

<400> 30

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PH-1064PCT-US seq.TXT

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Arg	Met	Arg	Arg	Met	Arg	Arg	Met	Trp	Ala	Thr	Gln	Gly	Leu	Ala	Val
	50		55		60										
Arg	Val	Ala	Leu	Ser	Val	Leu	Pro	Gly	Ser	Arg	Ala	Leu	Arg	Pro	Gly
	65		70		75										80
Asp	Cys	Glu	Val	Cys	Ile	Ser	Tyr	Leu	Gly	Arg	Phe	Tyr	Gln	Asp	Leu
			85		90									95	
Lys	Asp	Arg	Asp	Val	Thr	Phe	Ser	Pro	Ala	Thr	Ile	Glu	Asn	Glu	Leu
	100		105		110										
Ile	Lys	Phe	Cys	Arg	Glu	Ala	Arg	Gly	Lys	Glu	Asn	Arg	Leu	Cys	Tyr
	115		120		125										
Tyr	Ile	Gly	Ala	Thr	Asp	Asp	Ala	Ala	Thr	Lys	Ile	Ile	Asn	Glu	Val
	130		135		140										
Ser	Lys	Pro	Leu	Ala	His	His	Ile	Pro	Val	Glu	Lys	Ile	Cys	Glu	Lys
	145		150		155									160	
Leu	Lys	Lys	Lys	Asp	Ser	Gln	Ile	Cys	Glu	Leu	Lys	Tyr	Asp	Lys	Gln
			165		170									175	
Ile	Asp	Leu	Ser	Thr	Val	Asp	Leu	Lys	Lys	Leu	Arg	Val	Lys	Glu	Leu
	180		185		190										
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PH-1064PCT-US seq.TXT

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Pro Lys Ala Ala Ser Ala Pro Thr Asp Leu		
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<210> 31

<211> 1860

<212> DNA

<213> Homo sapiens

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<222> (94)..(1266)

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gag ccc gtc acg ctc ctg gtg aag agc ccc aac cag cgc cac cgc gac 162
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Val Lys Ser Pro Ser Lys Met Pro Glu Ile Asn Ala Lys Val Ala Glu	
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Ser Ala Gln Glu Ile Pro Val Val Ser Ala Pro Ala Pro Ala Pro Ile	
200 205 210 215	
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Pro Arg Pro Val Gln Asn Phe Pro Asn Asp Gly Pro Pro Pro Asp Val
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Val Asn Gln Asp Pro Asn Asn Asn Leu Gln Glu Gly Thr Asp Pro Glu
330 335 340

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Glu Gln Thr Ser Pro Ser Phe Met Ser Thr Ala Trp Leu Val Phe Lys
360 365 370 375

act ttc ttt gcc tct ctt ctt cca gaa ggc ccc cca gcc atc gca aac 1266
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380 385 390

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<211> 391

<212> PRT

<213> Homo sapiens

<400> 32

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Tyr Ala Arg Gln Tyr Tyr Met Gln Tyr Leu Ala Ala Thr Ala Ala Ser		
180	185	190
Gly Ala Phe Val Pro Pro Pro Ser Ala Gln Glu Ile Pro Val Val Ser		
195	200	205
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Asp Asp Glu Ile Asn Arg Asp Trp Leu Asp Trp Thr Tyr Ser Ala Ala		
260	265	270
Thr Phe Ser Val Phe Leu Ser Ile Leu Tyr Phe Tyr Ser Ser Leu Ser		
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Arg Phe Leu Met Val Met Gly Ala Thr Val Val Met Tyr Leu His His		
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Asp Arg Asp Val Leu Asp Gly Glu Gln Thr Ser Pro Ser Phe Met Ser						
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<210> 33

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<212> DNA

<213> Homo sapiens

<220>

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<222> (812)..(1138)

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 Glu Ser Ala Glu Glu Asp

105

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<213> Homo sapiens

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Arg	Gly	Arg	Pro	Lys	Gly	Ser	Lys	Asn	Lys	Ser	Pro	Ser	Lys	Ala	Ala
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<212> DNA

<213> Homo sapiens

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Met Glu His Gln Leu Leu Cys Cys Glu

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Val Glu Thr Ile Arg Arg Ala Tyr Pro Asp Ala Asn Leu Leu Asn Asp

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20

25

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Arg Val Leu Arg Ala Met Leu Lys Ala Glu Glu Thr Cys Ala Pro Ser

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Glu Lys Leu Cys Ile Tyr Thr Asp Asn Ser Ile Arg Pro Glu Glu Leu			
125	130	135	
ctg caa atg gag ctg ctc ctg gtg aac aag ctc aag tgg aac ctg gcc	606		
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Val Ala Leu Cys Ala Thr Asp Val Lys Phe Ile Ser Asn Pro Pro Ser
190                               195                               200
atg gtg gca gcg ggg agc gtg gtg gcc gca gtg caa ggc ctg aac ctg 798
Met Val Ala Ala Gly Ser Val Val Ala Ala Val Gln Gly Leu Asn Leu
205                               210                               215
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Arg Ser Pro Asn Asn Phe Leu Ser Tyr Tyr Arg Leu Thr Arg Phe Leu
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Asp Leu Ala Cys Thr Pro Thr Asp Val Arg Asp Val Asp Ile

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<211> 989

<212> PRT

<213> Homo sapiens

<400> 38

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PH-1064PCT-US seq.TXT

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Pro	Pro	Pro	Ser	Ser	Thr	Phe	Pro	Arg	Ile	His	Tyr	Asn	Ser	His	Phe				
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Thr Lys Asn Asn Thr Thr Glu Leu Thr Ala Pro Pro Pro Pro Pro Ala		
260	265	270
Pro Pro Ala Thr Cys Pro Ser Leu Gly Val Gly Thr Asp Thr Asn Tyr		
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Val Lys Arg Gly Ser Trp Ser Thr Leu Thr Leu Ser His Ala His Glu		
290	295	300
Val Cys Gln Lys Thr Ser Ala Thr Leu Asp Lys Ser Leu Leu Lys Ser		
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Lys Ser Cys His Gln Gly Leu Ala Tyr His Tyr Leu Gln Val Pro Gly		
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Gly Gly Gly Glu Trp Ser Thr Thr Leu Leu Ser Pro Arg Glu Thr Asp		
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Ala Ala Ala Glu Gly Pro Ile Pro Cys Arg Arg Met Arg Ser Gly Ser		
355	360	365
Tyr Ile Lys Ala Met Gly Asp Glu Asp Ser Asp Glu Ser Gly Gly Ser		
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Pro Lys Pro Ser Pro Lys Thr Ala Ala Arg Arg Gln Ser Tyr Leu Arg		
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Cys Ile Ser Gln Ile Phe Gly Gln Ala Ser Leu Ile Pro Gln Leu Phe		
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Gly His Glu Gln Gln Val Arg Glu Ala Glu Leu Ser Asp Gln Tyr Glu		
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Ala Ala Cys Glu Ser Ala Cys Ser Glu Ala Glu Ser Thr Ala Ala Glu		
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Thr Leu Asp Leu Pro Leu Pro Ser Tyr Phe Arg Ser Arg Ser His Ser		
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Tyr Leu Arg Ala Ile Gln Ala Gly Cys Ser Gln Glu Glu Asp Ser Val		
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Ser Leu Gln Ser Leu Ser Pro Pro Pro Ser Thr Gly Ser Leu Ser Asn		
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Ser Arg Thr Leu Pro Ser Ser Ser Cys Leu Val Ala Tyr Lys Lys Thr		
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Pro Pro Pro Val Pro Pro Arg Thr Thr Ser Lys Pro Phe Ile Ser Val		
565	570	575
Thr Val Gln Ser Ser Thr Glu Ser Ala Gln Asp Thr Tyr Leu Asp Ser		
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Glu Ala Ala Pro Lys Arg Lys Leu Ser Ser Ile Gly Ile Gln Glu Arg		
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Thr Arg Arg Asn Gly Ser His Leu Ser Glu Asp Asn Gly Pro Lys Ala		
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Ile Asp Val Met Ala Pro Ser Ser Glu Ser Ser Val Pro Ser His Ser		
690	695	700
Met Ser Ser Arg Arg Asp Thr Asp Ser Asp Thr Gln Asp Ala Asn Asp		
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Ser Ser Cys Lys Ser Ser Glu Arg Ser Leu Pro Asp Cys Thr Pro His		720
725	730	735
Pro Asn Ser Ile Ser Ile Asp Ala Gly Pro Arg Gln Ala Pro Lys Ile		
740	745	750
Ala Gln Ile Lys Arg Asn Leu Ser Tyr Gly Asp Asn Ser Asp Pro Ala		
755	760	765
Leu Glu Ala Ser Ser Leu Pro Pro Pro Asp Pro Trp Leu Glu Thr Ser		
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Gly Trp Cys Cys Gln Met Asp Lys Glu Thr Lys Glu Asn Asn Leu Ser						
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Glu Glu Val Leu Gly Lys Val Leu Ser Ala Val Gly Ser Ala Gln Leu						
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Leu Met Ser Gln Lys Phe Gln Gln Phe Arg Gly Leu Cys Glu Gln Asn						
	850		855		860	
Leu Asn Pro Asp Ala Asn Pro Arg Pro Thr Ala Gln Asp Leu Ala Gly						
865		870		875		880
Phe Trp Asp Leu Leu Gln Leu Ser Ile Glu Asp Ile Ser Met Lys Phe						
	885		890		895	
Asp Glu Leu Tyr His Leu Lys Ala Asn Ser Trp Gln Leu Val Glu Thr						
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Pro Glu Lys Arg Lys Glu Glu Lys Lys Pro Pro Pro Pro Val Pro Lys						
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Lys Pro Ala Lys Ser Lys Pro Ala Val Ser Arg Asp Lys Ala Ser Asp						
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Ala Ser Asp Lys Gln Arg Gln Glu Ala Arg Lys Arg Leu Leu Ala Ala						
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Lys Arg Ala Ala Ser Val Arg Gln Asn Ser Ala Thr Glu Ser Ala Asp						
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<211> 2522

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(1545)

<400> 39

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Gln Leu Gln Asp Glu Met Leu Arg Arg Val Asp Ala Glu Asn Arg Leu

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Gln Thr Met Lys Glu Glu Leu Asp Phe Gln Lys Asn Ile Tyr Ser Glu

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Ala Glu Arg Asn Ser Asn Leu Val Gly Ala Ala His Glu Glu Leu Gln				
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Glu Ser Thr Glu Ser Arg Ser Ser Phe Ser Gln His Ala Arg Thr Ser			
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Gly Arg Val Ala Val Glu Glu Val Asp Glu Glu Gly Lys Phe Val Arg			
290	295	300	
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385	390	395	400
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<212> PRT

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 405 410 415
 His Gly Ser His Cys Ser Ser Ser Gly Asp Pro Ala Glu Tyr Asn Leu
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 Arg Ser Arg Thr Val Leu Cys Gly Thr Cys Gly Gln Pro Ala Asp Lys
 435 440 445
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PH-1064PCT-US seq.TXT

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Gln Tyr Gly Pro Ser Ser Ala Ala Met Ala Trp Arg Arg Gly Ser Met
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Gly Asp Tyr Met Ala Gln Glu Asp Asp Trp Asp Arg Asp Leu Leu Leu
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Ile	Asn	Asn	Val	Asn	Lys	Ala	Leu	Asp	Phe	Ile	Ala	Ser	Lys	Gly	Ile	
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Lys	Leu	Asp	Phe	His	Arg	Ala	Glu	Glu	Ile	Val	Asp	Gly	Asn	Ala	Lys	
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His	Ile	Ser	Trp	Lys	Asp	Gly	Leu	Ala	Phe	Asn	Ala	Leu	Ile	His	Arg	
			190				195					200				
cac	aga	cca	gag	ctg	att	gag	tat	gac	aag	ctg	agg	aag	gac	gac	cct	734
His	Arg	Pro	Glu	Leu	Ile	Glu	Tyr	Asp	Lys	Leu	Arg	Lys	Asp	Asp	Pro	
			205				210					215				
gtc	acc	aac	ctg	aac	aat	gcc	ttc	gaa	gtg	gct	gag	aaa	tac	ctc	gac	782
Val	Thr	Asn	Leu	Asn	Asn	Ala	Phe	Glu	Val	Ala	Glu	Lys	Tyr	Leu	Asp	
			220			225				230				235		
atc	ccc	aag	atg	ctg	gat	gca	gag	gac	atc	gtg	aac	acg	gcc	cgg	ccc	830
Ile	Pro	Lys	Met	Leu	Asp	Ala	Glu	Asp	Ile	Val	Asn	Thr	Ala	Arg	Pro	
				240				245						250		
gac	gag	aag	gcc	ata	atg	acc	tat	gtg	tcc	agc	ttc	tac	cat	gcc	ttt	878
Asp	Glu	Lys	Ala	Ile	Met	Thr	Tyr	Val	Ser	Ser	Phe	Tyr	His	Ala	Phe	
			255					260						265		
tca	gga	gcg	cag	aag	gct	gaa	act	gaa	act	gcc	gcc	aac	cgg	atc	tgt	926
Ser	Gly	Ala	Gln	Lys	Ala	Glu	Thr	Glu	Thr	Ala	Ala	Asn	Arg	Ile	Cys	
			270				275					280				
aag	gtg	ctg	gct	gtc	aac	caa	gag	aac	tgc	agc	acc	tcg	atg	gag	gac	974
Lys	Val	Leu	Ala	Val	Asn	Gln	Glu	Asn	Cys	Ser	Thr	Ser	Met	Glu	Asp	
			285				290					295				
tac	gag	aag	ctg	gcc	agc	gac	ctc	ctg	gag	tgg	atc	cgg	cgc	acc	atc	1022

PH-1064PCT-US seq.TXT

Tyr	Glu	Lys	Leu	Ala	Ser	Asp	Leu	Leu	Glu	Trp	Ile	Arg	Arg	Thr	Ile		
300					305					310					315		
ccc	tgg	ctg	gag	gac	cgt	gtg	ccc	caa	aag	act	atc	cag	gag	atg	cag	1070	
Pro	Trp	Leu	Glu	Asp	Arg	Val	Pro	Gln	Lys	Thr	Ile	Gln	Glu	Met	Gln		
				320						325					330		
cag	aag	ctg	gag	gac	ttc	cgc	gac	tac	cgg	cgt	gtg	cac	aag	ccg	ccc	1118	
Gln	Lys	Leu	Glu	Asp	Phe	Arg	Asp	Tyr	Arg	Arg	Val	His	Lys	Pro	Pro		
				335						340					345		
aag	gtg	cag	gag	aag	tgc	cag	ctg	gag	atc	aac	ttc	aac	agc	gtg	cag	1166	
Lys	Val	Gln	Glu	Lys	Cys	Gln	Leu	Glu	Ile	Asn	Phe	Asn	Ser	Val	Gln		
				350						355					360		
acc	aag	ctg	cgc	ctc	agc	aac	cgg	ccc	gcc	ttc	atg	ccc	tcc	gag	ggc	1214	
Thr	Lys	Leu	Arg	Leu	Ser	Asn	Arg	Pro	Ala	Phe	Met	Pro	Ser	Glu	Gly		
				365						370					375		
aag	atg	gtc	tcg	gac	atc	aac	aat	ggc	tgg	cag	cac	ttg	gag	cag	gct	1262	
Lys	Met	Val	Ser	Asp	Ile	Asn	Asn	Gly	Trp	Gln	His	Leu	Glu	Gln	Ala		
380					385					390					395		
gag	aag	ggc	tac	gag	gag	tgg	ctg	ctg	aat	gag	att	cgc	agg	ctg	gag	1310	
Glu	Lys	Gly	Tyr	Glu	Glu	Trp	Leu	Leu	Asn	Glu	Ile	Arg	Arg	Leu	Glu		
				400						405					410		
cgg	ctc	gac	cac	ctg	gca	gag	aag	ttc	cgg	cag	aaa	gcc	tcc	atc	cac	1358	
Arg	Leu	Asp	His	Leu	Ala	Glu	Lys	Phe	Arg	Gln	Lys	Ala	Ser	Ile	His		
				415						420					425		
gag	gcc	tgg	act	gac	ggg	aag	gaa	gcc	atg	ctg	aag	cac	cgg	gac	tac	1406	

PH-1064PCT-US seq.TXT

Glu	Ala	Trp	Thr	Asp	Gly	Lys	Glu	Ala	Met	Leu	Lys	His	Arg	Asp	Tyr		
	430					435						440					
gag	acg	gcc	aca	cta	tcg	gac	atc	aaa	gcc	ctc	att	cgc	aag	cac	gag	1454	
Glu	Thr	Ala	Thr	Leu	Ser	Asp	Ile	Lys	Ala	Leu	Ile	Arg	Lys	His	Glu		
	445					450						455					
gcc	ttc	gag	agc	gac	ctg	gct	gcg	cac	cag	gac	cgc	gtg	gag	cag	atc	1502	
Ala	Phe	Glu	Ser	Asp	Leu	Ala	Ala	His	Gln	Asp	Arg	Val	Glu	Gln	Ile		
460					465					470				475			
gcc	gcc	tcc	gcc	cag	gag	ctc	aac	gag	ctg	gat	tac	tac	gac	tcc	cac	1550	
Ala	Ala	Ser	Ala	Gln	Glu	Leu	Asn	Glu	Leu	Asp	Tyr	Tyr	Asp	Ser	His		
				480						485				490			
aat	gtc	aac	acc	cgg	tgc	cag	aag	atc	tgt	gac	cag	tgg	gac	gcc	ctc	1598	
Asn	Val	Asn	Thr	Arg	Cys	Gln	Lys	Ile	Cys	Asp	Gln	Trp	Asp	Ala	Leu		
				495						500				505			
ggc	tct	ctg	aca	cat	agt	cgc	agg	gaa	gcc	ctg	gag	aaa	aca	gag	aag	1646	
Gly	Ser	Leu	Thr	His	Ser	Arg	Arg	Glu	Ala	Leu	Glu	Lys	Thr	Glu	Lys		
				510						515				520			
cag	ctg	gag	gcc	atc	atc	gac	cag	ctg	cac	ctg	gaa	tac	gcc	aag	ccc	1694	
Gln	Leu	Glu	Ala	Ile	Ile	Asp	Gln	Leu	His	Leu	Glu	Tyr	Ala	Lys	Pro		
				525						530				535			
gcg	gcc	ccc	ttc	aac	aac	tgg	atg	gag	agc	gcc	atg	gag	gac	ctc	cag	1742	
Ala	Ala	Pro	Phe	Asn	Asn	Trp	Met	Glu	Ser	Ala	Met	Glu	Asp	Leu	Gln		
540					545					550				555			
gac	atg	ttc	atc	gtc	cat	acc	atc	gag	gag	att	gag	ggc	ctg	atc	tca	1790	

PH-1064PCT-US seq.TXT

Asp Met Phe Ile Val His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser	
560	565
570	
gcc cat gac cag ttc aag tcc acc ctg ccg gac gcc gat agg gag cgc	1838
Ala His Asp Gln Phe Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg	
575	580
585	
gag gcc atc ctg cat cca caa gga ggc cag agg atc gct gag agc aac	1886
Glu Ala Ile Leu His Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn	
590	595
600	
cac atc aag ctg tcg ggc agc aac ccc tac acc acc gtc acc ccg caa	1934
His Ile Lys Leu Ser Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln	
605	610
615	
atc atc aac tcc aag tgg gag aag gtg cag cag ctg gtg cca aaa cgg	1982
Ile Ile Asn Ser Lys Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg	
620	625
630	635
gac cat gcc ctc ctg gag gag cag agc aag cag cag cag tcc aac gag	2030
Asp His Ala Leu Leu Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu	
640	645
650	
cac ctg cgc cgc cag ttc gcc agc cag gcc aat gtt gtg ggg ccc tgg	2078
His Leu Arg Arg Gln Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp	
655	660
665	
atc cag acc aag atg gag gag atc gcg atc tcc att gag atg aac ggg	2126
Ile Gln Thr Lys Met Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly	
670	675
680	
acc ctg gag gac cag ctg agc cac ctg aag cag tat gaa cgc agc atc	2174

PH-1064PCT-US seq.TXT

Thr	Leu	Glu	Asp	Gln	Leu	Ser	His	Leu	Lys	Gln	Tyr	Glu	Arg	Ser	Ile		
685						690						695					
gtg	gac	tac	aag	ccc	aac	ctg	gac	ctg	ctg	gag	cag	cag	cac	cag	ctc	2222	
Val	Asp	Tyr	Lys	Pro	Asn	Leu	Asp	Leu	Leu	Glu	Gln	Gln	His	Gln	Leu		
700					705					710					715		
atc	cag	gag	gcc	ctc	atc	ttc	gac	aac	aag	cac	acc	aac	tat	acc	atg	2270	
Ile	Gln	Glu	Ala	Leu	Ile	Phe	Asp	Asn	Lys	His	Thr	Asn	Tyr	Thr	Met		
				720						725					730		
gag	cac	atc	cgc	gtg	ggc	tgg	gag	cag	ctg	ctc	acc	acc	att	gcc	cgc	2318	
Glu	His	Ile	Arg	Val	Gly	Trp	Glu	Gln	Leu	Leu	Thr	Thr	Ile	Ala	Arg		
				735						740					745		
acc	atc	aac	gag	gtg	gag	aac	cag	atc	ctt	acc	cgc	gac	gcc	aag	ggc	2366	
Thr	Ile	Asn	Glu	Val	Glu	Asn	Gln	Ile	Leu	Thr	Arg	Asp	Ala	Lys	Gly		
				750						755					760		
atc	agc	cag	gag	cag	atg	cag	gag	ttc	cgg	gcg	tcc	ttc	aac	cac	ttc	2414	
Ile	Ser	Gln	Glu	Gln	Met	Gln	Glu	Phe	Arg	Ala	Ser	Phe	Asn	His	Phe		
				765						770					775		
gac	aag	gat	cat	ggc	ggg	gcg	ctg	ggg	cga	gga	gtt	caa	ggc	ctg	cct	2462	
Asp	Lys	Asp	His	Gly	Gly	Ala	Leu	Gly	Arg	Gly	Val	Gln	Gly	Leu	Pro		
780						785						790			795		
cat	cag	cct	ggg	cta	cga	cgt	gga	gaa	cga	ccg	gca	ggt	gag	gcc	gag	2510	
His	Gln	Pro	Gly	Leu	Arg	Arg	Gly	Glu	Arg	Pro	Ala	Gly	Glu	Ala	Glu		
				800						805					810		
ttc	aac	cgc	atc	atg	agc	ctg	gtc	gac	ccc	aac	cat	agc	ggc	ctt	gtt	2558	

PH-1064PCT-US seq.TXT

Phe Asn Arg Ile Met Ser Leu Val Asp Pro Asn His Ser Gly Leu Val
815 820 825
acc ttc caa gcc ttc atc gac ttc atg tcg cgg gag acc acc gac acc 2606
Thr Phe Gln Ala Phe Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr
830 835 840
gac acg gct gac cag gta atc act tcc ttc aag gtc cta gca ggg gac 2654
Asp Thr Ala Asp Gln Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp
845 850 855
aag aac ttc atc aca gct gag gag ctg cgg aga gag ctg ccc ccc gac 2702
Lys Asn Phe Ile Thr Ala Glu Glu Leu Arg Arg Glu Leu Pro Pro Asp
860 865 870 875
cag gcc gag tac tgc atc gcc cgc atg gcg cca tac cag ggc cct gac 2750
Gln Ala Glu Tyr Cys Ile Ala Arg Met Ala Pro Tyr Gln Gly Pro Asp
880 885 890
ggc gtg cgc ggt gcc ctc gac tac aag tcc ttc tcc acg gcc ttg tat 2798
Gly Val Arg Gly Ala Leu Asp Tyr Lys Ser Phe Ser Thr Ala Leu Tyr
895 900 905
ggc gag agc gac ctg tgaggcccca gagacctgac ccaacacccc cgacgcctcc 2853
Gly Glu Ser Asp Leu
910
aggagcctgg cagccccaca gtcccattcc tccactctgt atctatgcaa agcactctct 2913
ctgcagtctc cgggggtgggt ggggtgggcag ggaggggctg gggcaggctc tctcctctct 2973
ctctttgtgg gttggccagg aggttcccc gaccaggttg gggagacttg gggccagcgc 3033
ttctgggtctg gtaaatatgt atgatgtgtt gtgctttttt aaccaaggag gggccagtgg 3093

PH-1064PCT-US seq.TXT

attccacag cacaaccggt cccttccatg ccctgggatg cctcaccaca cccaggtctc 3153
 ttccctttgct ctgaggtccc ttcaaggcct cccaatcca ggccaaagcc ccatgtgcct 3213
 tgtccagggga actgcctggg ccatgcgagg ggccagcaga gggcgccacc acctgacggc 3273
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 tggccccaac aagcaccggt cttttgcagc agaggagctg agttggcaga ccgggcccc 3393
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 attttctaag aaccaaaaaa a 3474

<210> 42

<211> 912

<212> PRT

<213> Homo sapiens

<400> 42

Met	Val	Asp	Tyr	His	Ala	Ala	Asn	Gln	Ser	Tyr	Gln	Tyr	Gly	Pro	Ser
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Ser	Ala	Ala	Met	Ala	Trp	Arg	Arg	Gly	Ser	Met	Gly	Asp	Tyr	Met	Ala
				20				25					30		
Gln	Glu	Asp	Asp	Trp	Asp	Arg	Asp	Leu	Leu	Leu	Asp	Pro	Ala	Trp	Glu
				35				40					45		
Lys	Gln	Gln	Arg	Lys	Thr	Phe	Thr	Ala	Trp	Ser	Asn	Ser	His	Leu	Arg
				50				55					60		
Lys	Ala	Gly	Thr	Gln	Ile	Glu	Asn	Ile	Asp	Glu	Asp	Phe	Arg	Asp	Gly
				65				70					75		80
Leu	Lys	Leu	Met	Leu	Leu	Leu	Glu	Val	Ile	Ser	Gly	Glu	Arg	Leu	Pro
				85						90				95	

PH-1064PCT-US seq.TXT

Lys Pro Glu Arg Gly Lys Met Arg Val His Lys Ile Asn Asn Val Asn
 100 105 110
 Lys Ala Leu Asp Phe Ile Ala Ser Lys Gly Ile Lys Leu Asp Phe His
 115 120 125
 Arg Ala Glu Glu Ile Val Asp Gly Asn Ala Lys Met Thr Leu Gly Met
 130 135 140
 Ile Trp Thr Ile Ile Leu Arg Phe Ala Ile Gln Asp Ile Ser Val Glu
 145 150 155 160
 Glu Thr Ser Ala Lys Glu Gly Leu Leu Leu Trp Cys Gln Arg Lys Thr
 165 170 175
 Ala Pro Tyr Lys Asn Val Asn Val Gln Asn Phe His Ile Ser Trp Lys
 180 185 190
 Asp Gly Leu Ala Phe Asn Ala Leu Ile His Arg His Arg Pro Glu Leu
 195 200 205
 Ile Glu Tyr Asp Lys Leu Arg Lys Asp Asp Pro Val Thr Asn Leu Asn
 210 215 220
 Asn Ala Phe Glu Val Ala Glu Lys Tyr Leu Asp Ile Pro Lys Met Leu
 225 230 235 240
 Asp Ala Glu Asp Ile Val Asn Thr Ala Arg Pro Asp Glu Lys Ala Ile
 245 250 255
 Met Thr Tyr Val Ser Ser Phe Tyr His Ala Phe Ser Gly Ala Gln Lys
 260 265 270
 Ala Glu Thr Glu Thr Ala Ala Asn Arg Ile Cys Lys Val Leu Ala Val
 275 280 285

PH-1064PCT-US seq.TXT

Asn	Gln	Glu	Asn	Cys	Ser	Thr	Ser	Met	Glu	Asp	Tyr	Glu	Lys	Leu	Ala
290						295					300				
Ser	Asp	Leu	Leu	Glu	Trp	Ile	Arg	Arg	Thr	Ile	Pro	Trp	Leu	Glu	Asp
305					310					315					320
Arg	Val	Pro	Gln	Lys	Thr	Ile	Gln	Glu	Met	Gln	Gln	Lys	Leu	Glu	Asp
				325						330				335	
Phe	Arg	Asp	Tyr	Arg	Arg	Val	His	Lys	Pro	Pro	Lys	Val	Gln	Glu	Lys
			340						345				350		
Cys	Gln	Leu	Glu	Ile	Asn	Phe	Asn	Ser	Val	Gln	Thr	Lys	Leu	Arg	Leu
		355					360					365			
Ser	Asn	Arg	Pro	Ala	Phe	Met	Pro	Ser	Glu	Gly	Lys	Met	Val	Ser	Asp
		370				375					380				
Ile	Asn	Asn	Gly	Trp	Gln	His	Leu	Glu	Gln	Ala	Glu	Lys	Gly	Tyr	Glu
385					390					395					400
Glu	Trp	Leu	Leu	Asn	Glu	Ile	Arg	Arg	Leu	Glu	Arg	Leu	Asp	His	Leu
				405						410				415	
Ala	Glu	Lys	Phe	Arg	Gln	Lys	Ala	Ser	Ile	His	Glu	Ala	Trp	Thr	Asp
			420						425				430		
Gly	Lys	Glu	Ala	Met	Leu	Lys	His	Arg	Asp	Tyr	Glu	Thr	Ala	Thr	Leu
		435					440						445		
Ser	Asp	Ile	Lys	Ala	Leu	Ile	Arg	Lys	His	Glu	Ala	Phe	Glu	Ser	Asp
		450					455					460			
Leu	Ala	Ala	His	Gln	Asp	Arg	Val	Glu	Gln	Ile	Ala	Ala	Ser	Ala	Gln
465					470					475					480

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Glu Leu Asn Glu Leu Asp Tyr Tyr Asp Ser His Asn Val Asn Thr Arg			
485	490	495	
Cys Gln Lys Ile Cys Asp Gln Trp Asp Ala Leu Gly Ser Leu Thr His			
500	505	510	
Ser Arg Arg Glu Ala Leu Glu Lys Thr Glu Lys Gln Leu Glu Ala Ile			
515	520	525	
Ile Asp Gln Leu His Leu Glu Tyr Ala Lys Pro Ala Ala Pro Phe Asn			
530	535	540	
Asn Trp Met Glu Ser Ala Met Glu Asp Leu Gln Asp Met Phe Ile Val			
545	550	555	560
His Thr Ile Glu Glu Ile Glu Gly Leu Ile Ser Ala His Asp Gln Phe			
565	570	575	
Lys Ser Thr Leu Pro Asp Ala Asp Arg Glu Arg Glu Ala Ile Leu His			
580	585	590	
Pro Gln Gly Gly Gln Arg Ile Ala Glu Ser Asn His Ile Lys Leu Ser			
595	600	605	
Gly Ser Asn Pro Tyr Thr Thr Val Thr Pro Gln Ile Ile Asn Ser Lys			
610	615	620	
Trp Glu Lys Val Gln Gln Leu Val Pro Lys Arg Asp His Ala Leu Leu			
625	630	635	640
Glu Glu Gln Ser Lys Gln Gln Gln Ser Asn Glu His Leu Arg Arg Gln			
645	650	655	
Phe Ala Ser Gln Ala Asn Val Val Gly Pro Trp Ile Gln Thr Lys Met			
660	665	670	

PH-1064PCT-US seq.TXT

Glu Glu Ile Ala Ile Ser Ile Glu Met Asn Gly Thr Leu Glu Asp Gln			
675	680	685	
Leu Ser His Leu Lys Gln Tyr Glu Arg Ser Ile Val Asp Tyr Lys Pro			
690	695	700	
Asn Leu Asp Leu Leu Glu Gln Gln His Gln Leu Ile Gln Glu Ala Leu			
705	710	715	720
Ile Phe Asp Asn Lys His Thr Asn Tyr Thr Met Glu His Ile Arg Val			
725	730	735	
Gly Trp Glu Gln Leu Leu Thr Thr Ile Ala Arg Thr Ile Asn Glu Val			
740	745	750	
Glu Asn Gln Ile Leu Thr Arg Asp Ala Lys Gly Ile Ser Gln Glu Gln			
755	760	765	
Met Gln Glu Phe Arg Ala Ser Phe Asn His Phe Asp Lys Asp His Gly			
770	775	780	
Gly Ala Leu Gly Arg Gly Val Gln Gly Leu Pro His Gln Pro Gly Leu			
785	790	795	800
Arg Arg Gly Glu Arg Pro Ala Gly Glu Ala Glu Phe Asn Arg Ile Met			
805	810	815	
Ser Leu Val Asp Pro Asn His Ser Gly Leu Val Thr Phe Gln Ala Phe			
820	825	830	
Ile Asp Phe Met Ser Arg Glu Thr Thr Asp Thr Asp Thr Ala Asp Gln			
835	840	845	
Val Ile Thr Ser Phe Lys Val Leu Ala Gly Asp Lys Asn Phe Ile Thr			
850	855	860	

PH-1064PCT-US seq.TXT

Ala	Glu	Glu	Leu	Arg	Arg	Glu	Leu	Pro	Pro	Asp	Gln	Ala	Glu	Tyr	Cys
865					870					875					880
Ile	Ala	Arg	Met	Ala	Pro	Tyr	Gln	Gly	Pro	Asp	Gly	Val	Arg	Gly	Ala
				885					890					895	
Leu	Asp	Tyr	Lys	Ser	Phe	Ser	Thr	Ala	Leu	Tyr	Gly	Glu	Ser	Asp	Leu
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<210> 43

<211> 8971

<212> DNA

<213> Homo sapiens

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<221> CDS

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<400> 43

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Met Pro Ser

1

acg gag aag gac ctg gcg gag gac gcg ccg tgg aag aag atc cag cag 166
Thr Glu Lys Asp Leu Ala Glu Asp Ala Pro Trp Lys Lys Ile Gln Gln

5

10

15

aac aca ttc acg cgc tgg tgc aat gag cac ctc aag tgc gtg ggc aag 214
Asn Thr Phe Thr Arg Trp Cys Asn Glu His Leu Lys Cys Val Gly Lys

PH-1064PCT-US seq.TXT

20	25	30	35	
cgc ctg acc gac ctg cag cgc gac ctc agc gac ggg ctc cgg ctc atc	262			
Arg Leu Thr Asp Leu Gln Arg Asp Leu Ser Asp Gly Leu Arg Leu Ile				
40	45	50		
gcg ctg ctc gag gtg ctc agc cag aag cgc atg tac cgc aag ttc cat	310			
Ala Leu Leu Glu Val Leu Ser Gln Lys Arg Met Tyr Arg Lys Phe His				
55	60	65		
ccg cgc ccc aac ttc cgc caa atg aag ctg gag aac gtg tcc gtg gcc	358			
Pro Arg Pro Asn Phe Arg Gln Met Lys Leu Glu Asn Val Ser Val Ala				
70	75	80		
ctc gag ttc ctc gag cgc gag cac atc aag ctc gtg tcc ata gac agc	406			
Leu Glu Phe Leu Glu Arg Glu His Ile Lys Leu Val Ser Ile Asp Ser				
85	90	95		
aag gcc atc gtg gat ggg aac ctg aag ctg atc ctg ggc ctg atc tgg	454			
Lys Ala Ile Val Asp Gly Asn Leu Lys Leu Ile Leu Gly Leu Ile Trp				
100	105	110	115	
acg ctg atc ctg cac tac tcc atc tcc atg ccc atg tgg gag gat gaa	502			
Thr Leu Ile Leu His Tyr Ser Ile Ser Met Pro Met Trp Glu Asp Glu				
120	125	130		
gat gat gag gat gcc cgc aaa cag acg ccc aag cag cgg ctg ctt ggc	550			
Asp Asp Glu Asp Ala Arg Lys Gln Thr Pro Lys Gln Arg Leu Leu Gly				
135	140	145		
tgg atc cag aac aag gtg ccc cag ctg ccc atc acc aac ttc aac cgt	598			
Trp Ile Gln Asn Lys Val Pro Gln Leu Pro Ile Thr Asn Phe Asn Arg				

PH-1064PCT-US seq.TXT

150	155	160	
gac tgg cag gac ggc aaa gct ctg ggc gcc ctg gtg gac aac tgc gcc			646
Asp Trp Gln Asp Gly Lys Ala Leu Gly Ala Leu Val Asp Asn Cys Ala			
165	170	175	
ccc ggt ctc tgc ccc gac tgg gag gcc tgg gat ccc aac cag ccc gtg			694
Pro Gly Leu Cys Pro Asp Trp Glu Ala Trp Asp Pro Asn Gln Pro Val			
180	185	190	195
gag aac tcc cgg gag gcc atg cag cag gcc gac gac tgg ctt ggg gtg			742
Glu Asn Ser Arg Glu Ala Met Gln Gln Ala Asp Asp Trp Leu Gly Val			
200	205	210	
ccc cag gtc att gcc cct gag gag att gtg gac ccc aac gtg gat gag			790
Pro Gln Val Ile Ala Pro Glu Glu Ile Val Asp Pro Asn Val Asp Glu			
215	220	225	
cat tct gtt atg acc tac ctg tcc cag ttc ccc aag gcc aag ctc aaa			838
His Ser Val Met Thr Tyr Leu Ser Gln Phe Pro Lys Ala Lys Leu Lys			
230	235	240	
cct ggt gcc cct gtt cga tcc aag cag ctg aac ccc aag aaa gcc atc			886
Pro Gly Ala Pro Val Arg Ser Lys Gln Leu Asn Pro Lys Lys Ala Ile			
245	250	255	
gcc tat ggg cct ggc atc gag cca cag ggc aac acc gtg ctg cag cct			934
Ala Tyr Gly Pro Gly Ile Glu Pro Gln Gly Asn Thr Val Leu Gln Pro			
260	265	270	275
gcc cac ttc acc gtg cag acg gtg gac gcg ggc gtg ggc gag gtg ctg			982
Ala His Phe Thr Val Gln Thr Val Asp Ala Gly Val Gly Glu Val Leu			

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280	285	290	
gtc tac atc gag gac cct gaa ggc cac acc gag gag gct aag gtg gtt			1030
Val Tyr Ile Glu Asp Pro Glu Gly His Thr Glu Glu Ala Lys Val Val			
295	300	305	
ccc aac aat gac aag gat cgc acc tat gct gtc tcc tat gtg ccc aag			1078
Pro Asn Asn Asp Lys Asp Arg Thr Tyr Ala Val Ser Tyr Val Pro Lys			
310	315	320	
gtc gct ggg tta cac aag gtg acc gtg ctc ttt gct ggc cag aac att			1126
Val Ala Gly Leu His Lys Val Thr Val Leu Phe Ala Gly Gln Asn Ile			
325	330	335	
gaa cgc agt ccc ttt gag gtg aac gtg ggc atg gcc ctg gga gat gcc			1174
Glu Arg Ser Pro Phe Glu Val Asn Val Gly Met Ala Leu Gly Asp Ala			
340	345	350	355
aac aag gtg tca gcc cgt ggc cct ggc ctg gaa cct gtg ggc aat gtg			1222
Asn Lys Val Ser Ala Arg Gly Pro Gly Leu Glu Pro Val Gly Asn Val			
360	365	370	
gcc aac aaa ccc acc tac ttt gac atc tac act gcg ggg gcc ggc act			1270
Ala Asn Lys Pro Thr Tyr Phe Asp Ile Tyr Thr Ala Gly Ala Gly Thr			
375	380	385	
ggc gat gtt gct gtg gtg atc gtg gac cca cag ggc cgg cgg gac aca			1318
Gly Asp Val Ala Val Val Ile Val Asp Pro Gln Gly Arg Arg Asp Thr			
390	395	400	
gtg gag gtg gcc ctg gag gac aag ggt gac agc acg ttc cgc tgc aca			1366
Val Glu Val Ala Leu Glu Asp Lys Gly Asp Ser Thr Phe Arg Cys Thr			

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405	410	415	
tac aga cct gcc atg gag ggg cca cat acc gtg cat gtg gcc ttt gcg	1414		
Tyr Arg Pro Ala Met Glu Gly Pro His Thr Val His Val Ala Phe Ala			
420	425	430	435
ggt gcc ccc atc acc cgc agt ccc ttc cct gtc cat gtg tcg gaa gcc	1462		
Gly Ala Pro Ile Thr Arg Ser Pro Phe Pro Val His Val Ser Glu Ala			
440	445	450	
tgt aac ccc aac gcc tgc cgc gcc tct ggg cga ggc ctg cag ccc aag	1510		
Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu Gln Pro Lys			
455	460	465	
ggt gtt cgc gtg aaa gag gtg gct gac ttc aag gtg ttt acc aag ggt	1558		
Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe Thr Lys Gly			
470	475	480	
gcc ggc agc ggg gag ctc aag gtc acg gtc aag ggg cca aag ggc aca	1606		
Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro Lys Gly Thr			
485	490	495	
gag gag cca gtg aag gtg cgg gag gct ggg gat ggt gtg ttc gag tgc	1654		
Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val Phe Glu Cys			
500	505	510	515
gag tac tac ccg gtg gtg cct ggg aag tat gtg gtg acc atc acg tgg	1702		
Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr Ile Thr Trp			
520	525	530	
ggc ggc tac gcc atc cct cgc agc ccc ttt gag gta cag gtg agc cca	1750		
Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln Val Ser Pro			

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535	540	545	
gag gca gga gtg caa aag gtc cgg gcc tgg ggt cct ggt ttg gag act			1798
Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly Leu Glu Thr			
550	555	560	
ggc cag gtg ggc aag tca gcc gat ttt gtg gtg gaa gcc att ggc acc			1846
Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala Ile Gly Thr			
565	570	575	
gag gtg ggg aca ctg ggc ttc tcc atc gag ggg ccc tca caa gcc aag			1894
Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser Gln Ala Lys			
580	585	590	595
atc gaa tgt gac gat aag ggg gat ggc tcc tgc gat gtg cgg tac tgg			1942
Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val Arg Tyr Trp			
600	605	610	
ccc acg gag cct ggg gag tac gct gtg cac gtc atc tgt gac gat gag			1990
Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys Asp Asp Glu			
615	620	625	
gac atc cga gac tca ccc ttc att gcc cac atc ctg ccc gcc cca cct			2038
Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro Ala Pro Pro			
630	635	640	
gac tgc ttc cca gat aag gtg aag gcc ttt ggg cct ggc ctg gag cct			2086
Asp Cys Phe Pro Asp Lys Val Lys Ala Phe Gly Pro Gly Leu Glu Pro			
645	650	655	
acc ggc tgc atc gtg gac aag ccc gct gag ttc acc att gat gct cgt			2134
Thr Gly Cys Ile Val Asp Lys Pro Ala Glu Phe Thr Ile Asp Ala Arg			

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660	665	670	675	
gca gct ggc aag gga gac ctg aag ctc tat gcc cag gac gcc gac ggc				2182
Ala Ala Gly Lys Gly Asp Leu Lys Leu Tyr Ala Gln Asp Ala Asp Gly				
	680	685	690	
tgt ccc atc gac atc aag gtg atc ccc aac ggc aac ggc acc ttc cgc				2230
Cys Pro Ile Asp Ile Lys Val Ile Pro Asn Gly Asn Gly Thr Phe Arg				
	695	700	705	
tgc tcc tac gtg ccc acc aag ccc att aag cac acc atc atc atc tcc				2278
Cys Ser Tyr Val Pro Thr Lys Pro Ile Lys His Thr Ile Ile Ile Ser				
	710	715	720	
tgg gga ggc gta aac gtg ccc aag agc ccc ttc cgg gtg aac gtg ggc				2326
Trp Gly Gly Val Asn Val Pro Lys Ser Pro Phe Arg Val Asn Val Gly				
	725	730	735	
gag ggc agc cac ccc gag cgg gta aag gtg tac ggc ccc gga gtg gag				2374
Glu Gly Ser His Pro Glu Arg Val Lys Val Tyr Gly Pro Gly Val Glu				
740	745	750	755	
aag aca ggc ctc aag gcc aat gag ccc acc tac ttc acg gtg gac tgc				2422
Lys Thr Gly Leu Lys Ala Asn Glu Pro Thr Tyr Phe Thr Val Asp Cys				
	760	765	770	
agc gag gcg ggg caa ggc gac gtg agc atc ggc atc aag tgc gcc cca				2470
Ser Glu Ala Gly Gln Gly Asp Val Ser Ile Gly Ile Lys Cys Ala Pro				
	775	780	785	
ggc gtg gtg ggc cct gca gag gct gac att gac ttc gac atc atc aag				2518
Gly Val Val Gly Pro Ala Glu Ala Asp Ile Asp Phe Asp Ile Ile Lys				

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790                                795                                800
aat gac aac gac acc ttc acc gtc aag tac acg cca cca ggg gcg ggc 2566
Asn Asp Asn Asp Thr Phe Thr Val Lys Tyr Thr Pro Pro Gly Ala Gly
805                                810                                815
cgc tac acc atc atg gtg ctg ttt gcc aac cag gag atc ccc gcc agc 2614
Arg Tyr Thr Ile Met Val Leu Phe Ala Asn Gln Glu Ile Pro Ala Ser
820                                825                                830                                835
ccc ttc cac atc aag gtg gac cca tcc cac gat gcc agc aaa gtc aag 2662
Pro Phe His Ile Lys Val Asp Pro Ser His Asp Ala Ser Lys Val Lys
840                                845                                850
gcc gag ggc cct ggg ctg aat cgc aca ggt gtg gaa gtc ggg aag ccc 2710
Ala Glu Gly Pro Gly Leu Asn Arg Thr Gly Val Glu Val Gly Lys Pro
855                                860                                865
acc cac ttc acg gtg ctg acc aag gga gcc ggc aag gcc aag ctg gat 2758
Thr His Phe Thr Val Leu Thr Lys Gly Ala Gly Lys Ala Lys Leu Asp
870                                875                                880
gtg cag ttt gca ggg aca gcc aag ggc gag gtt gtg cgg gac ttt gag 2806
Val Gln Phe Ala Gly Thr Ala Lys Gly Glu Val Val Arg Asp Phe Glu
885                                890                                895
atc ata gac aac cat gac tac tcc tac act gtc aag tac acc gct gtc 2854
Ile Ile Asp Asn His Asp Tyr Ser Tyr Thr Val Lys Tyr Thr Ala Val
900                                905                                910                                915
cag cag ggc aac atg gca gtg aca gtg act tat ggc ggg gac cct gtc 2902
Gln Gln Gly Asn Met Ala Val Thr Val Thr Tyr Gly Gly Asp Pro Val

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920	925	930	
ccc aag agc ccc ttt gtg gtg aat gtg gca ccc ccg ctg gac ctc agc			2950
Pro Lys Ser Pro Phe Val Val Asn Val Ala Pro Pro Leu Asp Leu Ser			
935	940	945	
aaa atc aaa gtt cag ggc ctt aat agc aag gtg gct gtg gga cag gaa			2998
Lys Ile Lys Val Gln Gly Leu Asn Ser Lys Val Ala Val Gly Gln Glu			
950	955	960	
caa gca ttc tct gtg aac aca cga ggg gct ggc ggt cag ggc caa ctg			3046
Gln Ala Phe Ser Val Asn Thr Arg Gly Ala Gly Gly Gln Gly Gln Leu			
965	970	975	
gat gtg cgg atg act tcg ccc tct cgc cgg ccc atc ccc tgc aag ctg			3094
Asp Val Arg Met Thr Ser Pro Ser Arg Arg Pro Ile Pro Cys Lys Leu			
980	985	990	995
gag cca ggc ggt gga gcg gaa gcc cag gct gtg cgc tac atg ccc ccg			3142
Glu Pro Gly Gly Gly Ala Glu Ala Gln Ala Val Arg Tyr Met Pro Pro			
1000	1005	1010	
gag gag ggg ccc tac aag gtg gat atc acc tac gat ggt cac ccg gtg			3190
Glu Glu Gly Pro Tyr Lys Val Asp Ile Thr Tyr Asp Gly His Pro Val			
1015	1020	1025	
cct ggc agc ccg ttt gct gtg gag ggt gtc ctg ccc cct gat ccc tcc			3238
Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro Asp Pro Ser			
1030	1035	1040	
aag gtc tgt gct tat ggc ccg ggt ctc aag ggt gga ctg gta ggc acc			3286
Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu Val Gly Thr			

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1050 1055

1045			
ccc gcg cca ttc tcc atc gac acc aag ggg gct ggc aca ggt ggc ctg	3334		
Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr Gly Gly Leu			
1060	1065	1070	1075
ggg ctg acc gta gag ggc ccc tgc gag gcc aag atc gag tgc cag gac	3382		
Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu Cys Gln Asp			
	1080	1085	1090
aat ggt gat ggc tca tgt gct gtc agc tac ctg ccc acg gag cct ggc	3430		
Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr Glu Pro Gly			
	1095	1100	1105
gag tac acc atc aac atc ctg ttt gct gag gcc cac atc cct ggc tcg	3478		
Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile Pro Gly Ser			
	1110	1115	1120
ccc ttc aaa gcc acc att cgg cct gtg ttt gac ccg agc aag gtg cgg	3526		
Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser Lys Val Arg			
	1125	1130	1135
gcc agt gga ccg ggc ctg gag cgc ggc aag gtc ggt gag gca gcc acc	3574		
Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu Ala Ala Thr			
1140	1145	1150	1155
ttc act gtg gac tgc tca gag gca ggc gag gcg gag ctg acc att gag	3622		
Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu Thr Ile Glu			
	1160	1165	1170
atc ctg tcg gat gcc ggg gtc aag gcc gag gtg ctg atc cac aac aac	3670		
Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile His Asn Asn			

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1175	1180	1185	
gcg gat ggc acc tac cac atc acc tac agc cct gcc ttc cct ggc acc			3718
Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe Pro Gly Thr			
1190	1195	1200	
tac acc att acc atc aag tat ggc ggg cat ccc gtg ccc aaa ttc ccc			3766
Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro Lys Phe Pro			
1205	1210	1215	
acc cgt gtc cat gtg cag cct gcg gtc gat acc agt ggc gtc aag gtc			3814
Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly Val Lys Val			
1220	1225	1230	1235
tca ggg cct ggt gtt gag cca cac ggt gtc ctg cgg gag gtg acc act			3862
Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu Val Thr Thr			
1240	1245	1250	
gag ttc act gtg gat gca aga tcc cta aca gcc aca ggc ggc aac cac			3910
Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly Gly Asn His			
1255	1260	1265	
gtg acg gct cgt gtg ctc aac ccc tcg ggg gcc aag aca gac acc tat			3958
Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr Asp Thr Tyr			
1270	1275	1280	
gtg aca gac aat ggg gac ggc acc tac cga gtg cag tac acc gcc tac			4006
Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr Thr Ala Tyr			
1285	1290	1295	
gag gag ggc gtg cat ctg gtg gag gtc ctg tat gat gag gtc gct gtg			4054
Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu Val Ala Val			

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1300	1305	1310	1315	
ccc aag agc ccc ttc cga gtg ggc gtg acc gag ggc tgt gat ccc acc				4102
Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys Asp Pro Thr				
	1320	1325	1330	
cgc gtc cga gcc ttc ggg cca ggc ctg gag ggt ggc ttg gtc aac aag				4150
Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu Val Asn Lys				
	1335	1340	1345	
gcc aac cga ttc act gtg gag acc agg gga gcg ggc acc ggg ggc ctt				4198
Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr Gly Gly Leu				
	1350	1355	1360	
ggc cta gcc atc gag ggt ccc tcg gaa gcc aag atg tcc tgc aag gac				4246
Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser Cys Lys Asp				
	1365	1370	1375	
aac aag gat ggt agc tgc acc gtg gag tac atc ccc ttc act cct gga				4294
Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe Thr Pro Gly				
1380	1385	1390	1395	
gac tat gac gtc aac atc acc ttc ggg ggg cgg ccc atc cca ggg agc				4342
Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile Pro Gly Ser				
	1400	1405	1410	
ccg ttc cgc gtg cca gtg aag gat gtg gtg gac cct ggg aag gtg aag				4390
Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly Lys Val Lys				
	1415	1420	1425	
tgc tca ggg cca ggg ctg ggg gct ggt gtc agg gcc cgg gtt cct cag				4438
Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg Val Pro Gln				

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1430	1435	1440	
acc ttc aca gtg gac tgc agt caa gct ggc cgg gcg ccc ctg cag gtg			4486
Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro Leu Gln Val			
1445	1450	1455	
gct gtg ctg ggc ccc aca ggt gtg gcc gag cct gtg gag gtg cgg gac			4534
Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu Val Arg Asp			
1460	1465	1470	1475
aat gga gat ggc acc cac act gtc cac tac acc cca gcc act gac ggg			4582
Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala Thr Asp Gly			
	1480	1485	1490
ccc tac acg gta gcc gtc aag tat gct gac cag gag gtg cca cgc agc			4630
Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val Pro Arg Ser			
	1495	1500	1505
ccc ttc aag atc aag gtc ctc cca gct cat gat gcc agc aag gtg cgg			4678
Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser Lys Val Arg			
	1510	1515	1520
gcc agc ggg cca ggc ctc aac gcc tct ggc atc cct gcc agc ctg cct			4726
Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala Ser Leu Pro			
	1525	1530	1535
gtg gag ttc acc atc gac gca cgg gac gcg ggc gag ggg ttg ctc act			4774
Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly Leu Leu Thr			
1540	1545	1550	1555
gtc cag atc ttg ggc ccc gag ggt aag ccc aag aag gcc aac atc cgg			4822
Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala Asn Ile Arg			

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1560	1565	1570	
gac aat ggg gat ggc acg tac gct gtg tcc tac ctg ccg gac atg agt 4870			
Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro Asp Met Ser			
1575	1580	1585	
ggc cgg tac acc atc acc atc aag tat ggc ggt gat gag atc ccc tac 4918			
Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu Ile Pro Tyr			
1590	1595	1600	
tcg ccc ttc cgc atc cat gct ctg ccc act ggg gat gcc agc aag tgc 4966			
Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala Ser Lys Cys			
1605	1610	1615	
ctc gtc aca gtg tcc att gga ggc cat ggc ctg ggt gcc tgc ctg ggc 5014			
Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala Cys Leu Gly			
1620	1625	1630	1635
cct cga atc cag att ggg cag gag acg gtg atc acg gtg gat gcc aag 5062			
Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val Asp Ala Lys			
1640	1645	1650	
gca gcc ggt gag ggg aag gtg aca tgc acg gtg tcc acg ccg gat ggg 5110			
Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr Pro Asp Gly			
1655	1660	1665	
gca gag ctc gat gtg gat gtg gtt gag aac cat gac ggt acc ttt gac 5158			
Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly Thr Phe Asp			
1670	1675	1680	
atc tac tac aca gcg ccc gag ccg ggc aag tac gtc atc acc atc cgc 5206			
Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile Thr Ile Arg			

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1685	1690	1695	
ttc ggg ggt gag cac atc ccc aac agc ccc ttc cac gtg ctg gcg tgt			5254
Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val Leu Ala Cys			
1700	1705	1710	1715
gac ccc ctg ccg cac gag gag gag ccc tct gaa gtg cca cag ctg cgc			5302
Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro Gln Leu Arg			
	1720	1725	1730
cag ccc tac gct cct ccc cgg ccc ggc gcc cgc ccc aca cac tgg gcc			5350
Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr His Trp Ala			
	1735	1740	1745
aca gag gag cca gtg gtg cct gtg gag cca atg gag tcc atg ctg agg			5398
Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser Met Leu Arg			
	1750	1755	1760
ccc ttc aac ctg gtc atc ccc ttc gcg gtg cag aaa ggg gag ctc aca			5446
Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly Glu Leu Thr			
	1765	1770	1775
gga gag gtg cgg atg ccc tcg ggg aag acg gca cgg ccc aac atc acc			5494
Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro Asn Ile Thr			
1780	1785	1790	1795
gac aac aag gac ggc acc atc acg gtg agg tat gca ccc act gag aaa			5542
Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro Thr Glu Lys			
	1800	1805	1810
ggc ctg cac cag atg ggg atc aag tat gac ggc aac cac atc cct ggg			5590
Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His Ile Pro Gly			

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1815	1820	1825	
agc ccc tta cag ttc tat gtg gat gcc atc aac agc cgc cat gtc agt			5638
Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg His Val Ser			
1830	1835	1840	
gcc tat ggg cca ggc ctg agc cat ggc atg gtc aac aag cca gcc acc			5686
Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys Pro Ala Thr			
1845	1850	1855	
ttc act att gtc acc aaa gat gct gga gaa ggg ggt ctg tca ctg gcc			5734
Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu Ser Leu Ala			
1860	1865	1870	1875
gtg gag ggc cca tcc aag gca gag atc acc tgt aag gac aac aag gat			5782
Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp Asn Lys Asp			
1880	1885	1890	
ggc acc tgc acc gtg tcc tat ctg ccg act gcg cct gga gac tac agc			5830
Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly Asp Tyr Ser			
1895	1900	1905	
atc atc gtg cgc ttc gat gac aag cac atc ccg ggg agc ccc ttc aca			5878
Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser Pro Phe Thr			
1910	1915	1920	
gcc aag atc aca ggt gat gac tcc atg agg acc tca cag ctg aat gtg			5926
Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln Leu Asn Val			
1925	1930	1935	
ggc acc tcc acg gac gtg tca ctg aag atc acc gag agt gat ctg agc			5974
Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser Asp Leu Ser			

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1940	1945	1950	1955	
cag ctg acc gcc agc atc cgt gcc ccc tcg ggc aac gag gag ccc tgc				6022
Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu Glu Pro Cys				
	1960	1965	1970	
ctg ctg aag cgc ctg ccc aac cgg cac att ggg atc tcc ttc acc ccc				6070
Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser Phe Thr Pro				
	1975	1980	1985	
aag gag gtc ggg gag cac gtg gtg agc gtg cgc aag agt ggc aag cat				6118
Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser Gly Lys His				
	1990	1995	2000	
gtc acc aac agc ccc ttc aag atc ctg gtg ggg cca tct gag atc ggg				6166
Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser Glu Ile Gly				
	2005	2010	2015	
gac gcc agc aag gtg cgg gtc tgg ggc aag ggg ctt tcc gag gga cac				6214
Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser Glu Gly His				
	2020	2025	2030	2035
aca ttc cag gtg gca gag ttc atc gtg gac act cgc aat gca ggt tat				6262
Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn Ala Gly Tyr				
	2040	2045	2050	
ggg ggc ttg ggg ctg agt att gaa ggc cca agc aag gtg gac atc aac				6310
Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val Asp Ile Asn				
	2055	2060	2065	
tgt gag gac atg gag gac ggg aca tgc aaa gtc acc tac tgc ccc acc				6358
Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr Cys Pro Thr				

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2070	2075	2080	
gag ccc ggc acc tac atc atc aac atc aag ttt gct gac aag cac gtg			6406
Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp Lys His Val			
2085	2090	2095	
cct gga agc ccc ttc act gtg aag gtg acc ggc gag ggc cgc atg aag			6454
Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly Arg Met Lys			
2100	2105	2110	2115
gag agc atc acc cgg cgg aga cag gca cct tcc atc gcc acc atc ggc			6502
Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala Thr Ile Gly			
	2120	2125	2130
agc acc tgt gac ctc aac ctc aag atc cca gga aac tgg ttc cag atg			6550
Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp Phe Gln Met			
	2135	2140	2145
gtg tct gcc cag gag cgc ctg aca cgc acc ttc aca cgc agc agc cac			6598
Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg Ser Ser His			
2150	2155	2160	
acc tac acc cgc acg gag cgc acg gag atc agc aag acg cgg ggc ggg			6646
Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr Arg Gly Gly			
2165	2170	2175	
gag aca aag ccc gag gtg cgg gtg gag gag tcc acc cag gtc ggc ggg			6694
Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln Val Gly Gly			
2180	2185	2190	2195
gac ccc ttc cct gct gtg ttt ggg gac ttc ctg ggc cgg gag cgc ctg			6742
Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg Glu Arg Leu			

2200	2205	2210	
gga tcc ttc ggc agc atc acc cgg cag cag gag ggt gag gcc agc tct			6790
Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu Ala Ser Ser			
2215	2220	2225	
cag gac atg act gca cag gtg acc agc cca tcg ggc aag gtg gaa gcc			6838
Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys Val Glu Ala			
2230	2235	2240	
gca gag atc gtc gag ggc gag gac agc gcc tac agc gtc cgc ttt gtg			6886
Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val Arg Phe Val			
2245	2250	2255	
ccc cag gaa atg ggg ccc cat acg gtc gct gtc aag tac cgt ggc cag			6934
Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr Arg Gly Gln			
2260	2265	2270	2275
cac gtg ccc ggc agc ccc ttt cag ttc act gtg ggg ccg ctg ggt gaa			6982
His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro Leu Gly Glu			
2280	2285	2290	
ggt ggt gcc cac aag gtg cgg gcc gga cga gca ggg ctg gag cga ggt			7030
Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu Glu Arg Gly			
2295	2300	2305	
gtg gcc ggc gtg cca gcc gag ttc agc atc tgg acc cgg gag gct ggc			7078
Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg Glu Ala Gly			
2310	2315	2320	
gct ggg ggc ctg tcc att gct gtg gag ggt cct agc aaa gcg gag att			7126
Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys Ala Glu Ile			

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2325	2330	2335	
gca ttt gag gat cgc aaa gat ggc tcc tgc ggc gtc tcc tat gtc gtc			7174
Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser Tyr Val Val			
2340	2345	2350	2355
cag gaa cca ggt gac tat gag gtc tcc atc aag ttc aat gat gag cac			7222
Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn Asp Glu His			
	2360	2365	2370
atc cca gac agc ccc ttt gtg gtg cct gtg gcc tcc ctc tcg gat gac			7270
Ile Pro Asp Ser Pro Phe Val Val Pro Val Ala Ser Leu Ser Asp Asp			
	2375	2380	2385
gct cgc cgt ctc act gtc acc agc ctc cag gag acg ggg ctc aag gtg			7318
Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly Leu Lys Val			
	2390	2395	2400
aac cag cca gcg tcc ttt gcc gtg cag ctg aac ggt gcc cgg ggc gtg			7366
Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala Arg Gly Val			
	2405	2410	2415
att gat gcc cgg gtg cac aca ccc tcg ggg gct gtg gag gag tgc tac			7414
Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu Glu Cys Tyr			
2420	2425	2430	2435
gtc tct gag ctg gac agt gac aag cac acc atc cgc ttc atc ccc cac			7462
Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe Ile Pro His			
	2440	2445	2450
gag aat ggc gtc cac tcc atc gat gtc aag ttc aac ggt gcc cac atc			7510
Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly Ala His Ile			

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2455	2460	2465	
cct gga agt ccc ttc aag atc cgc gtt ggg gag cag agc cag gct ggg			7558
Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser Gln Ala Gly			
2470	2475	2480	
gac cca ggc ttg gtg tca gcc tac ggt cct ggg ctc gag gga ggc act			7606
Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu Gly Gly Thr			
2485	2490	2495	
acc ggt gtg tca tca gag ttc atc gtg aac acc ctg aat gcc ggc tcg			7654
Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn Ala Gly Ser			
2500	2505	2510	2515
ggg gcc ttg tct gtc acc att gat ggc ccc tcc aag gtg cag ctg gac			7702
Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val Gln Leu Asp			
2520	2525	2530	
tgt cgg gag tgt cct gag ggc cat gtg gtc act tat act ccc atg gcc			7750
Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr Pro Met Ala			
2535	2540	2545	
cct ggc aac tac ctc att gcc atc aag tac ggt ggc ccc cag cac atc			7798
Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro Gln His Ile			
2550	2555	2560	
gtg ggc agc ccc ttc aag gcc aag gtc act ggt ccg agg ctg tcc gga			7846
Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg Leu Ser Gly			
2565	2570	2575	
ggc cac agc ctt cac gaa aca tcc acg gtt ctg gtg gag act gtg acc			7894
Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu Thr Val Thr			

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2580	2585	2590	2595	
aag tcc tcc tca agc cgg ggc tcc agc tac agc tcc atc ccc aag ttc				7942
Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile Pro Lys Phe				
	2600	2605	2610	
tcc tca gat gcc agc aag gtg gtg act cgg ggc cct ggg ctg tcc cag				7990
Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly Leu Ser Gln				
	2615	2620	2625	
gcc ttc gtg ggc cag aag aac tcc ttc acc gtg gac tgc agc aaa gca				8038
Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys Ser Lys Ala				
	2630	2635	2640	
ggc acc aac atg atg atg gtg ggc gtg cac ggc ccc aag acc ccc tgt				8086
Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys Thr Pro Cys				
	2645	2650	2655	
gag gag gtg tac gtg aag cac atg ggg aac cgg gtg tac aat gtc acc				8134
Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr Asn Val Thr				
2660	2665	2670	2675	
tac act gtc aag gag aaa ggg gac tac atc ctc att gtc aag tgg ggt				8182
Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val Lys Trp Gly				
	2680	2685	2690	
gac gaa agt gtc cct gga agc ccc ttc aaa gtc aag gtc cct				8224
Asp Glu Ser Val Pro Gly Ser Pro Phe Lys Val Lys Val Pro				
	2695	2700	2705	
tgaatcccaa aagtgccctcc ccagcctcag cccccacctc cagccacaca cacattacac				8284
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acacctgcct tgggggtgaa gtgaaggccc agcctcccca cccaccgcg cccaggggt 8404
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<210> 44

<211> 2705

<212> PRT

<213> Homo sapiens

<400> 44

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Ile	Gln	Gln	Asn	Thr	Phe	Thr	Arg	Trp	Cys	Asn	Glu	His	Leu	Lys	Cys
			20					25					30		
Val	Gly	Lys	Arg	Leu	Thr	Asp	Leu	Gln	Arg	Asp	Leu	Ser	Asp	Gly	Leu
		35					40						45		
Arg	Leu	Ile	Ala	Leu	Leu	Glu	Val	Leu	Ser	Gln	Lys	Arg	Met	Tyr	Arg
	50					55						60			

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Lys	Phe	His	Pro	Arg	Pro	Asn	Phe	Arg	Gln	Met	Lys	Leu	Glu	Asn	Val
65					70					75					80
Ser	Val	Ala	Leu	Glu	Phe	Leu	Glu	Arg	Glu	His	Ile	Lys	Leu	Val	Ser
					85					90					95
Ile	Asp	Ser	Lys	Ala	Ile	Val	Asp	Gly	Asn	Leu	Lys	Leu	Ile	Leu	Gly
					100					105					110
Leu	Ile	Trp	Thr	Leu	Ile	Leu	His	Tyr	Ser	Ile	Ser	Met	Pro	Met	Trp
					115					120					125
Glu	Asp	Glu	Asp	Asp	Glu	Asp	Ala	Arg	Lys	Gln	Thr	Pro	Lys	Gln	Arg
					130					135					140
Leu	Leu	Gly	Trp	Ile	Gln	Asn	Lys	Val	Pro	Gln	Leu	Pro	Ile	Thr	Asn
145					150					155					160
Phe	Asn	Arg	Asp	Trp	Gln	Asp	Gly	Lys	Ala	Leu	Gly	Ala	Leu	Val	Asp
					165					170					175
Asn	Cys	Ala	Pro	Gly	Leu	Cys	Pro	Asp	Trp	Glu	Ala	Trp	Asp	Pro	Asn
					180					185					190
Gln	Pro	Val	Glu	Asn	Ser	Arg	Glu	Ala	Met	Gln	Gln	Ala	Asp	Asp	Trp
					195					200					205
Leu	Gly	Val	Pro	Gln	Val	Ile	Ala	Pro	Glu	Glu	Ile	Val	Asp	Pro	Asn
					210					215					220
Val	Asp	Glu	His	Ser	Val	Met	Thr	Tyr	Leu	Ser	Gln	Phe	Pro	Lys	Ala
225					230					235					240
Lys	Leu	Lys	Pro	Gly	Ala	Pro	Val	Arg	Ser	Lys	Gln	Leu	Asn	Pro	Lys
					245					250					255

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Lys	Ala	Ile	Ala	Tyr	Gly	Pro	Gly	Ile	Glu	Pro	Gln	Gly	Asn	Thr	Val
		260						265						270	
Leu	Gln	Pro	Ala	His	Phe	Thr	Val	Gln	Thr	Val	Asp	Ala	Gly	Val	Gly
		275						280						285	
Glu	Val	Leu	Val	Tyr	Ile	Glu	Asp	Pro	Glu	Gly	His	Thr	Glu	Glu	Ala
		290						295						300	
Lys	Val	Val	Pro	Asn	Asn	Asp	Lys	Asp	Arg	Thr	Tyr	Ala	Val	Ser	Tyr
305					310					315					320
Val	Pro	Lys	Val	Ala	Gly	Leu	His	Lys	Val	Thr	Val	Leu	Phe	Ala	Gly
				325						330					335
Gln	Asn	Ile	Glu	Arg	Ser	Pro	Phe	Glu	Val	Asn	Val	Gly	Met	Ala	Leu
			340							345					350
Gly	Asp	Ala	Asn	Lys	Val	Ser	Ala	Arg	Gly	Pro	Gly	Leu	Glu	Pro	Val
		355								360					365
Gly	Asn	Val	Ala	Asn	Lys	Pro	Thr	Tyr	Phe	Asp	Ile	Tyr	Thr	Ala	Gly
		370								375					380
Ala	Gly	Thr	Gly	Asp	Val	Ala	Val	Val	Ile	Val	Asp	Pro	Gln	Gly	Arg
385					390							395			400
Arg	Asp	Thr	Val	Glu	Val	Ala	Leu	Glu	Asp	Lys	Gly	Asp	Ser	Thr	Phe
				405						410					415
Arg	Cys	Thr	Tyr	Arg	Pro	Ala	Met	Glu	Gly	Pro	His	Thr	Val	His	Val
				420						425					430
Ala	Phe	Ala	Gly	Ala	Pro	Ile	Thr	Arg	Ser	Pro	Phe	Pro	Val	His	Val
		435								440					445

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Ser Glu Ala Cys Asn Pro Asn Ala Cys Arg Ala Ser Gly Arg Gly Leu
450 455 460
Gln Pro Lys Gly Val Arg Val Lys Glu Val Ala Asp Phe Lys Val Phe
465 470 475 480
Thr Lys Gly Ala Gly Ser Gly Glu Leu Lys Val Thr Val Lys Gly Pro
485 490 495
Lys Gly Thr Glu Glu Pro Val Lys Val Arg Glu Ala Gly Asp Gly Val
500 505 510
Phe Glu Cys Glu Tyr Tyr Pro Val Val Pro Gly Lys Tyr Val Val Thr
515 520 525
Ile Thr Trp Gly Gly Tyr Ala Ile Pro Arg Ser Pro Phe Glu Val Gln
530 535 540
Val Ser Pro Glu Ala Gly Val Gln Lys Val Arg Ala Trp Gly Pro Gly
545 550 555 560
Leu Glu Thr Gly Gln Val Gly Lys Ser Ala Asp Phe Val Val Glu Ala
565 570 575
Ile Gly Thr Glu Val Gly Thr Leu Gly Phe Ser Ile Glu Gly Pro Ser
580 585 590
Gln Ala Lys Ile Glu Cys Asp Asp Lys Gly Asp Gly Ser Cys Asp Val
595 600 605
Arg Tyr Trp Pro Thr Glu Pro Gly Glu Tyr Ala Val His Val Ile Cys
610 615 620
Asp Asp Glu Asp Ile Arg Asp Ser Pro Phe Ile Ala His Ile Leu Pro
625 630 635 640

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Ala	Pro	Pro	Asp	Cys	Phe	Pro	Asp	Lys	Val	Lys	Ala	Phe	Gly	Pro	Gly
				645					650					655	
Leu	Glu	Pro	Thr	Gly	Cys	Ile	Val	Asp	Lys	Pro	Ala	Glu	Phe	Thr	Ile
				660					665					670	
Asp	Ala	Arg	Ala	Ala	Gly	Lys	Gly	Asp	Leu	Lys	Leu	Tyr	Ala	Gln	Asp
				675					680					685	
Ala	Asp	Gly	Cys	Pro	Ile	Asp	Ile	Lys	Val	Ile	Pro	Asn	Gly	Asn	Gly
				690					695					700	
Thr	Phe	Arg	Cys	Ser	Tyr	Val	Pro	Thr	Lys	Pro	Ile	Lys	His	Thr	Ile
705						710					715				720
Ile	Ile	Ser	Trp	Gly	Gly	Val	Asn	Val	Pro	Lys	Ser	Pro	Phe	Arg	Val
				725						730				735	
Asn	Val	Gly	Glu	Gly	Ser	His	Pro	Glu	Arg	Val	Lys	Val	Tyr	Gly	Pro
				740						745				750	
Gly	Val	Glu	Lys	Thr	Gly	Leu	Lys	Ala	Asn	Glu	Pro	Thr	Tyr	Phe	Thr
				755						760				765	
Val	Asp	Cys	Ser	Glu	Ala	Gly	Gln	Gly	Asp	Val	Ser	Ile	Gly	Ile	Lys
				770					775					780	
Cys	Ala	Pro	Gly	Val	Val	Gly	Pro	Ala	Glu	Ala	Asp	Ile	Asp	Phe	Asp
785						790					795				800
Ile	Ile	Lys	Asn	Asp	Asn	Asp	Thr	Phe	Thr	Val	Lys	Tyr	Thr	Pro	Pro
				805						810				815	
Gly	Ala	Gly	Arg	Tyr	Thr	Ile	Met	Val	Leu	Phe	Ala	Asn	Gln	Glu	Ile
				820						825				830	

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Pro	Ala	Ser	Pro	Phe	His	Ile	Lys	Val	Asp	Pro	Ser	His	Asp	Ala	Ser
		835					840					845			
Lys	Val	Lys	Ala	Glu	Gly	Pro	Gly	Leu	Asn	Arg	Thr	Gly	Val	Glu	Val
		850				855						860			
Gly	Lys	Pro	Thr	His	Phe	Thr	Val	Leu	Thr	Lys	Gly	Ala	Gly	Lys	Ala
865					870					875					880
Lys	Leu	Asp	Val	Gln	Phe	Ala	Gly	Thr	Ala	Lys	Gly	Glu	Val	Val	Arg
				885					890					895	
Asp	Phe	Glu	Ile	Ile	Asp	Asn	His	Asp	Tyr	Ser	Tyr	Thr	Val	Lys	Tyr
		900						905					910		
Thr	Ala	Val	Gln	Gln	Gly	Asn	Met	Ala	Val	Thr	Val	Thr	Tyr	Gly	Gly
		915				920						925			
Asp	Pro	Val	Pro	Lys	Ser	Pro	Phe	Val	Val	Asn	Val	Ala	Pro	Pro	Leu
		930				935						940			
Asp	Leu	Ser	Lys	Ile	Lys	Val	Gln	Gly	Leu	Asn	Ser	Lys	Val	Ala	Val
945					950					955					960
Gly	Gln	Glu	Gln	Ala	Phe	Ser	Val	Asn	Thr	Arg	Gly	Ala	Gly	Gly	Gln
				965					970					975	
Gly	Gln	Leu	Asp	Val	Arg	Met	Thr	Ser	Pro	Ser	Arg	Arg	Pro	Ile	Pro
		980						985					990		
Cys	Lys	Leu	Glu	Pro	Gly	Gly	Gly	Ala	Glu	Ala	Gln	Ala	Val	Arg	Tyr
		995					1000					1005			
Met	Pro	Pro	Glu	Glu	Gly	Pro	Tyr	Lys	Val	Asp	Ile	Thr	Tyr	Asp	Gly
		1010				1015						1020			

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His Pro Val Pro Gly Ser Pro Phe Ala Val Glu Gly Val Leu Pro Pro
 1025 1030 1035 1040
 Asp Pro Ser Lys Val Cys Ala Tyr Gly Pro Gly Leu Lys Gly Gly Leu
 1045 1050 1055
 Val Gly Thr Pro Ala Pro Phe Ser Ile Asp Thr Lys Gly Ala Gly Thr
 1060 1065 1070
 Gly Gly Leu Gly Leu Thr Val Glu Gly Pro Cys Glu Ala Lys Ile Glu
 1075 1080 1085
 Cys Gln Asp Asn Gly Asp Gly Ser Cys Ala Val Ser Tyr Leu Pro Thr
 1090 1095 1100
 Glu Pro Gly Glu Tyr Thr Ile Asn Ile Leu Phe Ala Glu Ala His Ile
 1105 1110 1115 1120
 Pro Gly Ser Pro Phe Lys Ala Thr Ile Arg Pro Val Phe Asp Pro Ser
 1125 1130 1135
 Lys Val Arg Ala Ser Gly Pro Gly Leu Glu Arg Gly Lys Val Gly Glu
 1140 1145 1150
 Ala Ala Thr Phe Thr Val Asp Cys Ser Glu Ala Gly Glu Ala Glu Leu
 1155 1160 1165
 Thr Ile Glu Ile Leu Ser Asp Ala Gly Val Lys Ala Glu Val Leu Ile
 1170 1175 1180
 His Asn Asn Ala Asp Gly Thr Tyr His Ile Thr Tyr Ser Pro Ala Phe
 1185 1190 1195 1200
 Pro Gly Thr Tyr Thr Ile Thr Ile Lys Tyr Gly Gly His Pro Val Pro
 1205 1210 1215

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Lys Phe Pro Thr Arg Val His Val Gln Pro Ala Val Asp Thr Ser Gly			
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Val Lys Val Ser Gly Pro Gly Val Glu Pro His Gly Val Leu Arg Glu			
1235	1240	1245	
Val Thr Thr Glu Phe Thr Val Asp Ala Arg Ser Leu Thr Ala Thr Gly			
1250	1255	1260	
Gly Asn His Val Thr Ala Arg Val Leu Asn Pro Ser Gly Ala Lys Thr			
1265	1270	1275	1280
Asp Thr Tyr Val Thr Asp Asn Gly Asp Gly Thr Tyr Arg Val Gln Tyr			
1285	1290	1295	
Thr Ala Tyr Glu Glu Gly Val His Leu Val Glu Val Leu Tyr Asp Glu			
1300	1305	1310	
Val Ala Val Pro Lys Ser Pro Phe Arg Val Gly Val Thr Glu Gly Cys			
1315	1320	1325	
Asp Pro Thr Arg Val Arg Ala Phe Gly Pro Gly Leu Glu Gly Gly Leu			
1330	1335	1340	
Val Asn Lys Ala Asn Arg Phe Thr Val Glu Thr Arg Gly Ala Gly Thr			
1345	1350	1355	1360
Gly Gly Leu Gly Leu Ala Ile Glu Gly Pro Ser Glu Ala Lys Met Ser			
1365	1370	1375	
Cys Lys Asp Asn Lys Asp Gly Ser Cys Thr Val Glu Tyr Ile Pro Phe			
1380	1385	1390	
Thr Pro Gly Asp Tyr Asp Val Asn Ile Thr Phe Gly Gly Arg Pro Ile			
1395	1400	1405	

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Pro Gly Ser Pro Phe Arg Val Pro Val Lys Asp Val Val Asp Pro Gly
1410 1415 1420
Lys Val Lys Cys Ser Gly Pro Gly Leu Gly Ala Gly Val Arg Ala Arg
1425 1430 1435 1440
Val Pro Gln Thr Phe Thr Val Asp Cys Ser Gln Ala Gly Arg Ala Pro
1445 1450 1455
Leu Gln Val Ala Val Leu Gly Pro Thr Gly Val Ala Glu Pro Val Glu
1460 1465 1470
Val Arg Asp Asn Gly Asp Gly Thr His Thr Val His Tyr Thr Pro Ala
1475 1480 1485
Thr Asp Gly Pro Tyr Thr Val Ala Val Lys Tyr Ala Asp Gln Glu Val
1490 1495 1500
Pro Arg Ser Pro Phe Lys Ile Lys Val Leu Pro Ala His Asp Ala Ser
1505 1510 1515 1520
Lys Val Arg Ala Ser Gly Pro Gly Leu Asn Ala Ser Gly Ile Pro Ala
1525 1530 1535
Ser Leu Pro Val Glu Phe Thr Ile Asp Ala Arg Asp Ala Gly Glu Gly
1540 1545 1550
Leu Leu Thr Val Gln Ile Leu Gly Pro Glu Gly Lys Pro Lys Lys Ala
1555 1560 1565
Asn Ile Arg Asp Asn Gly Asp Gly Thr Tyr Ala Val Ser Tyr Leu Pro
1570 1575 1580
Asp Met Ser Gly Arg Tyr Thr Ile Thr Ile Lys Tyr Gly Gly Asp Glu
1585 1590 1595 1600

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Ile Pro Tyr Ser Pro Phe Arg Ile His Ala Leu Pro Thr Gly Asp Ala			
	1605	1610	1615
Ser Lys Cys Leu Val Thr Val Ser Ile Gly Gly His Gly Leu Gly Ala			
	1620	1625	1630
Cys Leu Gly Pro Arg Ile Gln Ile Gly Gln Glu Thr Val Ile Thr Val			
	1635	1640	1645
Asp Ala Lys Ala Ala Gly Glu Gly Lys Val Thr Cys Thr Val Ser Thr			
	1650	1655	1660
Pro Asp Gly Ala Glu Leu Asp Val Asp Val Val Glu Asn His Asp Gly			
1665	1670	1675	1680
Thr Phe Asp Ile Tyr Tyr Thr Ala Pro Glu Pro Gly Lys Tyr Val Ile			
	1685	1690	1695
Thr Ile Arg Phe Gly Gly Glu His Ile Pro Asn Ser Pro Phe His Val			
	1700	1705	1710
Leu Ala Cys Asp Pro Leu Pro His Glu Glu Glu Pro Ser Glu Val Pro			
	1715	1720	1725
Gln Leu Arg Gln Pro Tyr Ala Pro Pro Arg Pro Gly Ala Arg Pro Thr			
	1730	1735	1740
His Trp Ala Thr Glu Glu Pro Val Val Pro Val Glu Pro Met Glu Ser			
1745	1750	1755	1760
Met Leu Arg Pro Phe Asn Leu Val Ile Pro Phe Ala Val Gln Lys Gly			
	1765	1770	1775
Glu Leu Thr Gly Glu Val Arg Met Pro Ser Gly Lys Thr Ala Arg Pro			
	1780	1785	1790

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Asn Ile Thr Asp Asn Lys Asp Gly Thr Ile Thr Val Arg Tyr Ala Pro			
1795	1800	1805	
Thr Glu Lys Gly Leu His Gln Met Gly Ile Lys Tyr Asp Gly Asn His			
1810	1815	1820	
Ile Pro Gly Ser Pro Leu Gln Phe Tyr Val Asp Ala Ile Asn Ser Arg			
1825	1830	1835	1840
His Val Ser Ala Tyr Gly Pro Gly Leu Ser His Gly Met Val Asn Lys			
1845	1850	1855	
Pro Ala Thr Phe Thr Ile Val Thr Lys Asp Ala Gly Glu Gly Gly Leu			
1860	1865	1870	
Ser Leu Ala Val Glu Gly Pro Ser Lys Ala Glu Ile Thr Cys Lys Asp			
1875	1880	1885	
Asn Lys Asp Gly Thr Cys Thr Val Ser Tyr Leu Pro Thr Ala Pro Gly			
1890	1895	1900	
Asp Tyr Ser Ile Ile Val Arg Phe Asp Asp Lys His Ile Pro Gly Ser			
1905	1910	1915	1920
Pro Phe Thr Ala Lys Ile Thr Gly Asp Asp Ser Met Arg Thr Ser Gln			
1925	1930	1935	
Leu Asn Val Gly Thr Ser Thr Asp Val Ser Leu Lys Ile Thr Glu Ser			
1940	1945	1950	
Asp Leu Ser Gln Leu Thr Ala Ser Ile Arg Ala Pro Ser Gly Asn Glu			
1955	1960	1965	
Glu Pro Cys Leu Leu Lys Arg Leu Pro Asn Arg His Ile Gly Ile Ser			
1970	1975	1980	

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Phe Thr Pro Lys Glu Val Gly Glu His Val Val Ser Val Arg Lys Ser			
1985	1990	1995	2000
Gly Lys His Val Thr Asn Ser Pro Phe Lys Ile Leu Val Gly Pro Ser			
	2005	2010	2015
Glu Ile Gly Asp Ala Ser Lys Val Arg Val Trp Gly Lys Gly Leu Ser			
	2020	2025	2030
Glu Gly His Thr Phe Gln Val Ala Glu Phe Ile Val Asp Thr Arg Asn			
	2035	2040	2045
Ala Gly Tyr Gly Gly Leu Gly Leu Ser Ile Glu Gly Pro Ser Lys Val			
	2050	2055	2060
Asp Ile Asn Cys Glu Asp Met Glu Asp Gly Thr Cys Lys Val Thr Tyr			
2065	2070	2075	2080
Cys Pro Thr Glu Pro Gly Thr Tyr Ile Ile Asn Ile Lys Phe Ala Asp			
	2085	2090	2095
Lys His Val Pro Gly Ser Pro Phe Thr Val Lys Val Thr Gly Glu Gly			
	2100	2105	2110
Arg Met Lys Glu Ser Ile Thr Arg Arg Arg Gln Ala Pro Ser Ile Ala			
	2115	2120	2125
Thr Ile Gly Ser Thr Cys Asp Leu Asn Leu Lys Ile Pro Gly Asn Trp			
	2130	2135	2140
Phe Gln Met Val Ser Ala Gln Glu Arg Leu Thr Arg Thr Phe Thr Arg			
2145	2150	2155	2160
Ser Ser His Thr Tyr Thr Arg Thr Glu Arg Thr Glu Ile Ser Lys Thr			
	2165	2170	2175

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Arg Gly Gly Glu Thr Lys Pro Glu Val Arg Val Glu Glu Ser Thr Gln			
2180	2185	2190	
Val Gly Gly Asp Pro Phe Pro Ala Val Phe Gly Asp Phe Leu Gly Arg			
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Glu Arg Leu Gly Ser Phe Gly Ser Ile Thr Arg Gln Gln Glu Gly Glu			
2210	2215	2220	
Ala Ser Ser Gln Asp Met Thr Ala Gln Val Thr Ser Pro Ser Gly Lys			
2225	2230	2235	2240
Val Glu Ala Ala Glu Ile Val Glu Gly Glu Asp Ser Ala Tyr Ser Val			
2245	2250	2255	
Arg Phe Val Pro Gln Glu Met Gly Pro His Thr Val Ala Val Lys Tyr			
2260	2265	2270	
Arg Gly Gln His Val Pro Gly Ser Pro Phe Gln Phe Thr Val Gly Pro			
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Leu Gly Glu Gly Gly Ala His Lys Val Arg Ala Gly Arg Ala Gly Leu			
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Glu Arg Gly Val Ala Gly Val Pro Ala Glu Phe Ser Ile Trp Thr Arg			
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Glu Ala Gly Ala Gly Gly Leu Ser Ile Ala Val Glu Gly Pro Ser Lys			
2325	2330	2335	
Ala Glu Ile Ala Phe Glu Asp Arg Lys Asp Gly Ser Cys Gly Val Ser			
2340	2345	2350	
Tyr Val Val Gln Glu Pro Gly Asp Tyr Glu Val Ser Ile Lys Phe Asn			
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Ser Asp Asp Ala Arg Arg Leu Thr Val Thr Ser Leu Gln Glu Thr Gly			
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Leu Lys Val Asn Gln Pro Ala Ser Phe Ala Val Gln Leu Asn Gly Ala			
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Arg Gly Val Ile Asp Ala Arg Val His Thr Pro Ser Gly Ala Val Glu			
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Glu Cys Tyr Val Ser Glu Leu Asp Ser Asp Lys His Thr Ile Arg Phe			
2435	2440	2445	
Ile Pro His Glu Asn Gly Val His Ser Ile Asp Val Lys Phe Asn Gly			
2450	2455	2460	
Ala His Ile Pro Gly Ser Pro Phe Lys Ile Arg Val Gly Glu Gln Ser			
2465	2470	2475	2480
Gln Ala Gly Asp Pro Gly Leu Val Ser Ala Tyr Gly Pro Gly Leu Glu			
2485	2490	2495	
Gly Gly Thr Thr Gly Val Ser Ser Glu Phe Ile Val Asn Thr Leu Asn			
2500	2505	2510	
Ala Gly Ser Gly Ala Leu Ser Val Thr Ile Asp Gly Pro Ser Lys Val			
2515	2520	2525	
Gln Leu Asp Cys Arg Glu Cys Pro Glu Gly His Val Val Thr Tyr Thr			
2530	2535	2540	
Pro Met Ala Pro Gly Asn Tyr Leu Ile Ala Ile Lys Tyr Gly Gly Pro			
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Gln His Ile Val Gly Ser Pro Phe Lys Ala Lys Val Thr Gly Pro Arg			
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Leu Ser Gly Gly His Ser Leu His Glu Thr Ser Thr Val Leu Val Glu			
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Thr Val Thr Lys Ser Ser Ser Ser Arg Gly Ser Ser Tyr Ser Ser Ile			
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Pro Lys Phe Ser Ser Asp Ala Ser Lys Val Val Thr Arg Gly Pro Gly			
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Leu Ser Gln Ala Phe Val Gly Gln Lys Asn Ser Phe Thr Val Asp Cys			
2625	2630	2635	2640
Ser Lys Ala Gly Thr Asn Met Met Met Val Gly Val His Gly Pro Lys			
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Thr Pro Cys Glu Glu Val Tyr Val Lys His Met Gly Asn Arg Val Tyr			
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Asn Val Thr Tyr Thr Val Lys Glu Lys Gly Asp Tyr Ile Leu Ile Val			
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Pro			
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<211> 2016

<212> DNA

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<213> Homo sapiens

<220>

<221> CDS

<222> (210)..(1352)

<400> 45

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Met Ser Ser Arg Ile Ala Arg Ala

1

5

ctc gcc tta gtc gtc acc ctt ctc cac ttg acc agg ctg gcg ctc tcc 281
 Leu Ala Leu Val Val Thr Leu Leu His Leu Thr Arg Leu Ala Leu Ser

10

15

20

acc tgc ccc gct gcc tgc cac tgc ccc ctg gag gcg ccc aag tgc gcg 329
 Thr Cys Pro Ala Ala Cys His Cys Pro Leu Glu Ala Pro Lys Cys Ala

25

30

35

40

ccg gga gtc ggg ctg gtc cgg gac ggc tgc ggc tgc tgt aag gtc tgc 377
 Pro Gly Val Gly Leu Val Arg Asp Gly Cys Gly Cys Cys Lys Val Cys

45

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gcc aag cag ctc aac gag gac tgc agc aaa acg cag ccc tgc gac cac 425
 Ala Lys Gln Leu Asn Glu Asp Cys Ser Lys Thr Gln Pro Cys Asp His

60

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70

acc aag ggg ctg gaa tgc aac ttc ggc gcc agc tcc acc gct ctg aag 473

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Gly	Ile	Cys	Arg	Ala	Gln	Ser	Glu	Gly	Arg	Pro	Cys	Glu	Tyr	Asn	Ser		
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aga	atc	tac	caa	aac	ggg	gaa	agt	ttc	cag	ccc	aac	tgt	aaa	cat	cag	569	
Arg	Ile	Tyr	Gln	Asn	Gly	Glu	Ser	Phe	Gln	Pro	Asn	Cys	Lys	His	Gln		
105						110					115				120		
tgc	aca	tgt	att	gat	ggc	gcc	gtg	ggc	tgc	att	cct	ctg	tgt	ccc	caa	617	
Cys	Thr	Cys	Ile	Asp	Gly	Ala	Val	Gly	Cys	Ile	Pro	Leu	Cys	Pro	Gln		
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gaa	cta	tct	ctc	ccc	aac	ttg	ggc	tgt	ccc	aac	cct	cgg	ctg	gtc	aaa	665	
Glu	Leu	Ser	Leu	Pro	Asn	Leu	Gly	Cys	Pro	Asn	Pro	Arg	Leu	Val	Lys		
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Val	Thr	Gly	Gln	Cys	Cys	Glu	Glu	Trp	Val	Cys	Asp	Glu	Asp	Ser	Ile		
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aag	gac	ccc	atg	gag	gac	cag	gac	ggc	ctc	ctt	ggc	aag	gag	ctg	gga	761	
Lys	Asp	Pro	Met	Glu	Asp	Gln	Asp	Gly	Leu	Leu	Gly	Lys	Glu	Leu	Gly		
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ttc	gat	gcc	tcc	gag	gtg	gag	ttg	acg	aga	aac	aat	gaa	ttg	att	gca	809	
Phe	Asp	Ala	Ser	Glu	Val	Glu	Leu	Thr	Arg	Asn	Asn	Glu	Leu	Ile	Ala		
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gtt	gga	aaa	ggc	agc	tca	ctg	aag	cgg	ctc	cct	gtt	ttt	gga	atg	gag	857	

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Pro Arg Ile Leu Tyr Asn Pro Leu Gln Gly Gln Lys Cys Ile Val Gln	
220	225
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Thr Thr Ser Trp Ser Gln Cys Ser Lys Thr Cys Gly Thr Gly Ile Ser	
235	240
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Thr Arg Val Thr Asn Asp Asn Pro Glu Cys Arg Leu Val Lys Glu Thr	
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Arg Ile Cys Glu Val Arg Pro Cys Gly Gln Pro Val Tyr Ser Ser Leu	
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275	280
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Lys Lys Gly Lys Lys Cys Ser Lys Thr Lys Lys Ser Pro Glu Pro Val	
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295	
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Arg Phe Thr Tyr Ala Gly Cys Leu Ser Val Lys Lys Tyr Arg Pro Lys	
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310	
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Tyr Cys Gly Ser Cys Val Asp Gly Arg Cys Cys Thr Pro Gln Leu Thr	
315	320
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PH-1064PCT-US seq.TXT

Arg Thr Val Lys Met Arg Phe Arg Cys Glu Asp Gly Glu Thr Phe Ser

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Lys Asn Val Met Met Ile Gln Ser Cys Lys Cys Asn Tyr Asn Cys Pro

345

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355

360

cat gcc aat gaa gca gcg ttt ccc ttc tac agg ctg ttc aat gac att 1337

His Ala Asn Glu Ala Ala Phe Pro Phe Tyr Arg Leu Phe Asn Asp Ile

365

370

375

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His Lys Phe Arg Asp

380

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gggactcatt gtagaaagga agccttgctc attcttgagg agcattaagg tatttcgaaa 1512

ctgccaaagg tgctggtgcg gatggacact aatgcagcca cgattggaga atactttgct 1572

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<210> 46

<211> 381

PH-1064PCT-US seq.TXT

<212> PRT

<213> Homo sapiens

<400> 46

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			20					25					30		
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Arg Leu Pro Val Phe Gly Met Glu Pro Arg Ile Leu Tyr Asn Pro Leu		
210	215	220
Gln Gly Gln Lys Cys Ile Val Gln Thr Thr Ser Trp Ser Gln Cys Ser		
225	230	235
Lys Thr Cys Gly Thr Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Pro		
245	250	255
Glu Cys Arg Leu Val Lys Glu Thr Arg Ile Cys Glu Val Arg Pro Cys		
260	265	270
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275	280	285
Thr Lys Lys Ser Pro Glu Pro Val Arg Phe Thr Tyr Ala Gly Cys Leu		
290	295	300
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305	310	315
Arg Cys Cys Thr Pro Gln Leu Thr Arg Thr Val Lys Met Arg Phe Arg		
325	330	335
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Cys Lys Cys Asn Tyr Asn Cys Pro His Ala Asn Glu Ala Ala Phe Pro		

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370 375 380

<210> 47

<211> 2743

<212> DNA

<213> Homo sapiens

<220>

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<222> (240)..(2387)

<400> 47

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cgcgcgggcg tgagcccggg gcgagggctg tcttcccgga gacccgaccc cggcagcgcg 180
gggcggccac ttctcctgtg cctccgcccc ctgctccact ccccgccgcc gccgcgcgg 239
atg cca agc acc agc ttt cca gtc cct tcc aag ttt cca ctt ggc cct 287
Met Pro Ser Thr Ser Phe Pro Val Pro Ser Lys Phe Pro Leu Gly Pro

1 5 10 15

gcg gct gcg gtc ttc ggg aga gga gaa act ttg ggg ccc gcg ccg cgc 335
Ala Ala Ala Val Phe Gly Arg Gly Glu Thr Leu Gly Pro Ala Pro Arg

20 25 30

gcc ggc ggc acc atg aag tca gcg gag gaa gaa cac tat ggc tat gca 383
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala

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ctg ccg gcc ccg tgc cac aac ctt cag acc tcc aca ccg ggc atc atc			479
Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile			
65	70	75	80
ccg ccg gcg gat cac ccc tcg ggg tac gga gca gct ttg gac ggt ggg			527
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly			
	85	90	95
ccc gcg ggc tac ttc ctc tcc tcc ggc cac acc agg cct gat ggg gcc			575
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala			
	100	105	110
cct gcc ctg gag agt cct cgc atc gag ata acc tcg tgc ttg ggc ctg			623
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu			
	115	120	125
tac cac aac aat aac cag ttt ttc cac gat gtg gag gtg gaa gac gtc			671
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val			
	130	135	140
ctc cct agc tcc aaa cgg tcc ccc tcc acg gcc acg ctg agt ctg ccc			719
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro			
145	150	155	160
agc ctg gag gcc tac aga gac ccc tcg tgc ctg agc ccg gcc agc agc			767
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser			

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Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro			
195	200	205	
tgc gtg tct ccc aag acc acg gac ccc gag gag ggc ttt ccc cgc ggg			911
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly			
210	215	220	
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Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr			
225	230	235	240
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Ser Pro Arg Ala Ser Val Thr Glu Glu Ser Trp Leu Gly Ala Arg Ser			
245	250	255	
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Ser Arg Pro Ala Ser Pro Cys Asn Lys Arg Lys Tyr Ser Leu Asn Gly			
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Arg Gln Pro Pro Tyr Ser Pro His His Ser Pro Thr Pro Ser Pro His			
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290
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325 330 335
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Lys Thr Thr Leu Glu Gln Pro Pro Ser Val Ala Leu Lys Val Glu Pro
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Val Gly Glu Asp Leu Gly Ser Pro Pro Pro Pro Ala Asp Phe Ala Pro
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Glu Asp Tyr Ser Ser Phe Gln His Ile Arg Lys Gly Gly Phe Cys Asp
370 375 380
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Gln Tyr Leu Ala Val Pro Gln His Pro Tyr Gln Trp Ala Lys Pro Lys
385 390 395 400
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Pro Leu Ser Pro Thr Ser Tyr Met Ser Pro Thr Leu Pro Ala Leu Asp
405 410 415
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Trp Gln Leu Pro Ser His Ser Gly Pro Tyr Glu Leu Arg Ile Glu Val

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Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg			
435	440	445	
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Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His			
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ggc tac ttg gag aat gag ccg ctg atg ctg cag ctt ttc att ggg acg			1679
Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr			
465	470	475	480
gcg gac gac cgc ctg ctg cgc ccg cac gcc ttc tac cag gtg cac cgc			1727
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg			
485	490	495	
atc aca ggg aag acc gtg tcc acc acc agc cac gag gct atc ctc tcc			1775
Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser			
500	505	510	
aac acc aaa gtc ctg gag atc cca ctc ctg ccg gag aac agc atg cga			1823
Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg			
515	520	525	
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Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile			
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Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val			

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Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala				
	580	585	590	
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Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val				
	595	600	605	
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Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp				
	610	615	620	
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Ser Lys Val Ile Phe Val Glu Lys Ala Pro Asp Gly His His Val Trp				
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Glu Met Glu Ala Lys Thr Asp Arg Asp Leu Cys Lys Pro Asn Ser Leu				
	645	650	655	
gtg gtt gag atc ccg cca ttt cgg aat cag agg ata acc agc ccc gtt				2255
Val Val Glu Ile Pro Pro Phe Arg Asn Gln Arg Ile Thr Ser Pro Val				
	660	665	670	
cac gtc agt ttc tac gtc tgc aac ggg aag aga aag cga agc cag tac				2303
His Val Ser Phe Tyr Val Cys Asn Gly Lys Arg Lys Arg Ser Gln Tyr				

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690                               695                               700
gta agc cgt gaa cat gag cgc gtg ggg tgc ttt ttc taaagacgca 2397
Val Ser Arg Glu His Glu Arg Val Gly Cys Phe Phe

705                               710                               715
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tagtgagacc gagccatcga tgccctgaaa aggaaaggaa aagggaagct tcggatgcat 2517
tttccttgat ccctgttggg ggtggggggc ggggggttgca tactcagata gtcacggtta 2577
ttttgcttct tgcgaatgta taacagccaa ggggaaaaca tggctcttct gctccaaaaa 2637
actgaggggg tcctggtgtg catttgcacc ctaaagctgc ttacggtgaa aaggcaaata 2697
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<210> 48

<211> 716

<212> PRT

<213> Homo sapiens

<400> 48

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                20                25                30
Ala Gly Gly Thr Met Lys Ser Ala Glu Glu Glu His Tyr Gly Tyr Ala
                35                40                45

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PH-1064PCT-US seq.TXT

Ser Ser Asn Val Ser Pro Ala Leu Pro Leu Pro Thr Ala His Ser Thr
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Leu Pro Ala Pro Cys His Asn Leu Gln Thr Ser Thr Pro Gly Ile Ile
65 70 75 80
Pro Pro Ala Asp His Pro Ser Gly Tyr Gly Ala Ala Leu Asp Gly Gly
85 90 95
Pro Ala Gly Tyr Phe Leu Ser Ser Gly His Thr Arg Pro Asp Gly Ala
100 105 110
Pro Ala Leu Glu Ser Pro Arg Ile Glu Ile Thr Ser Cys Leu Gly Leu
115 120 125
Tyr His Asn Asn Asn Gln Phe Phe His Asp Val Glu Val Glu Asp Val
130 135 140
Leu Pro Ser Ser Lys Arg Ser Pro Ser Thr Ala Thr Leu Ser Leu Pro
145 150 155 160
Ser Leu Glu Ala Tyr Arg Asp Pro Ser Cys Leu Ser Pro Ala Ser Ser
165 170 175
Leu Ser Ser Arg Ser Cys Asn Ser Glu Ala Ser Ser Tyr Glu Ser Asn
180 185 190
Tyr Ser Tyr Pro Tyr Ala Ser Pro Gln Thr Ser Pro Trp Gln Ser Pro
195 200 205
Cys Val Ser Pro Lys Thr Thr Asp Pro Glu Glu Gly Phe Pro Arg Gly
210 215 220
Leu Gly Ala Cys Thr Leu Leu Gly Ser Pro Gln His Ser Pro Ser Thr
225 230 235 240

PH-1064PCT-US seq.TXT

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				260					265					270	
Arg	Gln	Pro	Pro	Tyr	Ser	Pro	His	His	Ser	Pro	Thr	Pro	Ser	Pro	His
				275					280					285	
Gly	Ser	Pro	Arg	Val	Ser	Val	Thr	Asp	Asp	Ser	Trp	Leu	Gly	Asn	Thr
				290					295					300	
Thr	Gln	Tyr	Thr	Ser	Ser	Ala	Ile	Val	Ala	Ala	Ile	Asn	Ala	Leu	Thr
305						310					315				320
Thr	Asp	Ser	Ser	Leu	Asp	Leu	Gly	Asp	Gly	Val	Pro	Val	Lys	Ser	Arg
						325					330				335
Lys	Thr	Thr	Leu	Glu	Gln	Pro	Pro	Ser	Val	Ala	Leu	Lys	Val	Glu	Pro
						340								350	
Val	Gly	Glu	Asp	Leu	Gly	Ser	Pro	Pro	Pro	Pro	Ala	Asp	Phe	Ala	Pro
						355								365	
Glu	Asp	Tyr	Ser	Ser	Phe	Gln	His	Ile	Arg	Lys	Gly	Gly	Phe	Cys	Asp
						370								380	
Gln	Tyr	Leu	Ala	Val	Pro	Gln	His	Pro	Tyr	Gln	Trp	Ala	Lys	Pro	Lys
385						390								395	400
Pro	Leu	Ser	Pro	Thr	Ser	Tyr	Met	Ser	Pro	Thr	Leu	Pro	Ala	Leu	Asp
						405								410	415
Trp	Gln	Leu	Pro	Ser	His	Ser	Gly	Pro	Tyr	Glu	Leu	Arg	Ile	Glu	Val
						420								425	430

PH-1064PCT-US seq.TXT

Gln Pro Lys Ser His His Arg Ala His Tyr Glu Thr Glu Gly Ser Arg
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Gly Ala Val Lys Ala Ser Ala Gly Gly His Pro Ile Val Gln Leu His
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Gly Tyr Leu Glu Asn Glu Pro Leu Met Leu Gln Leu Phe Ile Gly Thr
465 470 475 480
Ala Asp Asp Arg Leu Leu Arg Pro His Ala Phe Tyr Gln Val His Arg
485 490 495
Ile Thr Gly Lys Thr Val Ser Thr Thr Ser His Glu Ala Ile Leu Ser
500 505 510
Asn Thr Lys Val Leu Glu Ile Pro Leu Leu Pro Glu Asn Ser Met Arg
515 520 525
Ala Val Ile Asp Cys Ala Gly Ile Leu Lys Leu Arg Asn Ser Asp Ile
530 535 540
Glu Leu Arg Lys Gly Glu Thr Asp Ile Gly Arg Lys Asn Thr Arg Val
545 550 555 560
Arg Leu Val Phe Arg Val His Val Pro Gln Pro Ser Gly Arg Thr Leu
565 570 575
Ser Leu Gln Val Ala Ser Asn Pro Ile Glu Cys Ser Gln Arg Ser Ala
580 585 590
Gln Glu Leu Pro Leu Val Glu Lys Gln Ser Thr Asp Ser Tyr Pro Val
595 600 605
Val Gly Gly Lys Lys Met Val Leu Ser Gly His Asn Phe Leu Gln Asp
610 615 620

PH-1064PCT-US seq.TXT

Ser	Lys	Val	Ile	Phe	Val	Glu	Lys	Ala	Pro	Asp	Gly	His	His	Val	Trp
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Glu	Met	Glu	Ala	Lys	Thr	Asp	Arg	Asp	Leu	Cys	Lys	Pro	Asn	Ser	Leu
				645					650					655	
Val	Val	Glu	Ile	Pro	Pro	Phe	Arg	Asn	Gln	Arg	Ile	Thr	Ser	Pro	Val
				660					665					670	
His	Val	Ser	Phe	Tyr	Val	Cys	Asn	Gly	Lys	Arg	Lys	Arg	Ser	Gln	Tyr
		675						680					685		
Gln	Arg	Phe	Thr	Tyr	Leu	Pro	Ala	Asn	Gly	Asn	Ala	Ile	Phe	Leu	Thr
	690						695						700		
Val	Ser	Arg	Glu	His	Glu	Arg	Val	Gly	Cys	Phe	Phe				
705						710							715		

<210> 49

<211> 2353

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (241)..(1482)

<400> 49

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ccgcccgctc	gccgccttcc	tcctctgcc	ttccttcccc	acggccggcc	gcctcctcgc	180

PH-1064PCT-US seq.TXT

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Met Ala Ser Gly Asp Thr Leu Tyr Ile Ala Thr Asp Gly Ser Glu Met
    1             5             10             15
ccg gcc gag atc gtg gag ctg cac gag atc gag gtg gag acc atc ccg 336
Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
            20             25             30
gtg gag acc atc gag acc aca gtg gtg ggc gag gag gag gag gag gac 384
Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Glu Asp
            35             40             45
gac gac gac gag gac ggc ggc ggt ggc gac cac ggc ggc ggg ggc ggc 432
Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
            50             55             60
cac ggg cac gcc ggc cac cac cac cac cac cat cac cac cac cac cac 480
His Gly His Ala Gly His His His His His His His His His His His
            65             70             75             80
ccg ccc atg atc gct ctg cag ccg ctg gtc acc gac gac ccg acc cag 528
Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln
            85             90             95
gtg cac cac cac cag gag gtg atc ctg gtg cag acg cgc gag gag gtg 576
Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
            100            105            110
gtg ggc ggc gac gac tcg gac ggg ctg cgc gcc gag gac ggc ttc gag 624
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu

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PH-1064PCT-US seq.TXT

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Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp			
130	135	140	
tac att gaa caa acg ctg gtc acc gtg gcg gcg gcc ggc aag agc ggc			720
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly			
145	150	155	160
ggc ggc ggc tcg tcg tcg tcg gga ggc ggc cgc gtc aag aag ggc ggc			768
Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly			
165	170	175	
ggc aag aag agc ggc aag aag agt tac ctc agc ggc ggc gcc ggc gcg			816
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala			
180	185	190	
gcg ggc ggc cgc ggc gcc gac ccg ggc aac aag aag tgg gag cag aag			864
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys			
195	200	205	
cag gtg cag atc aag acc ctg gag ggc gag ttc tcg gtc acc atg tgg			912
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp			
210	215	220	
tcc tca gat gaa aaa aaa gat att gac cat gag aca gtg gtt gaa gaa			960
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu			
225	230	235	240
cag atc att gga gag aac tca cct cct gat tat tca gaa tat atg aca			1008
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr			

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245	250	255	
gga aag aaa ctt cct cct gga gga ata cct ggc att gac ctc tca gat	1056		
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp			
260	265	270	
ccc aaa caa ctg gca gaa ttt gct aga atg aag cca aga aaa att aaa	1104		
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys			
275	280	285	
gaa gat gat gct cca aga aca ata gct tgc cct cat aaa ggc tgc aca	1152		
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr			
290	295	300	
aag atg ttc agg gat aac tcg gcc atg aga aaa cat ctg cac acc cac	1200		
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His			
305	310	315	320
ggt ccc aga gtc cac gtc tgt gca gaa tgt ggc aaa gct ttt gtt gag	1248		
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu			
325	330	335	
agt tca aaa cta aaa cga cac caa ctg gtt cat act gga gag aag ccc	1296		
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro			
340	345	350	
ttt cag tgc acg ttc gaa ggc tgt ggg aaa cgc ttt tca ctg gac ttc	1344		
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe			
355	360	365	
aat ttg cgc aca cat gtg cga atc cat acc gga gac agg ccc tat gtg	1392		
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val			

370 tgc ccc ttc gat ggt tgt aat aag aag ttt gct cag tca act aac ctg 1440
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu
385 390 395 400
aaa tct cac atc tta aca cat gct aag gcc aaa aac aac cag 1482
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln
405 410
tgaaaagaag agagaagacc cttctcgacc acgggaagca tcttccagaa gtgtgattgg 1542
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aatactgcca gatgctgatg ttcagtgtaa tttctttgcc tgttcagtta cagaaagtgg 2262
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aaagggcaac aataaaatag caatcctaaa g 2353

<210> 50

<211> 414

PH-1064PCT-US seq.TXT

<212> PRT

<213> Homo sapiens

<400> 50

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Pro Ala Glu Ile Val Glu Leu His Glu Ile Glu Val Glu Thr Ile Pro
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Val Glu Thr Ile Glu Thr Thr Val Val Gly Glu Glu Glu Glu Asp
      35             40             45
Asp Asp Asp Glu Asp Gly Gly Gly Gly Asp His Gly Gly Gly Gly Gly
      50             55             60
His Gly His Ala Gly His His His His His His His His His His His
      65             70             75             80
Pro Pro Met Ile Ala Leu Gln Pro Leu Val Thr Asp Asp Pro Thr Gln
      85             90             95
Val His His His Gln Glu Val Ile Leu Val Gln Thr Arg Glu Glu Val
      100            105            110
Val Gly Gly Asp Asp Ser Asp Gly Leu Arg Ala Glu Asp Gly Phe Glu
      115            120            125
Asp Gln Ile Leu Ile Pro Val Pro Ala Pro Ala Gly Gly Asp Asp Asp
      130            135            140
Tyr Ile Glu Gln Thr Leu Val Thr Val Ala Ala Ala Gly Lys Ser Gly
      145            150            155            160
Gly Gly Gly Ser Ser Ser Ser Gly Gly Gly Arg Val Lys Lys Gly Gly

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PH-1064PCT-US seq.TXT

165	170	175
Gly Lys Lys Ser Gly Lys Lys Ser Tyr Leu Ser Gly Gly Ala Gly Ala		
180	185	190
Ala Gly Gly Arg Gly Ala Asp Pro Gly Asn Lys Lys Trp Glu Gln Lys		
195	200	205
Gln Val Gln Ile Lys Thr Leu Glu Gly Glu Phe Ser Val Thr Met Trp		
210	215	220
Ser Ser Asp Glu Lys Lys Asp Ile Asp His Glu Thr Val Val Glu Glu		
225	230	235
Gln Ile Ile Gly Glu Asn Ser Pro Pro Asp Tyr Ser Glu Tyr Met Thr		
245	250	255
Gly Lys Lys Leu Pro Pro Gly Gly Ile Pro Gly Ile Asp Leu Ser Asp		
260	265	270
Pro Lys Gln Leu Ala Glu Phe Ala Arg Met Lys Pro Arg Lys Ile Lys		
275	280	285
Glu Asp Asp Ala Pro Arg Thr Ile Ala Cys Pro His Lys Gly Cys Thr		
290	295	300
Lys Met Phe Arg Asp Asn Ser Ala Met Arg Lys His Leu His Thr His		
305	310	315
Gly Pro Arg Val His Val Cys Ala Glu Cys Gly Lys Ala Phe Val Glu		
325	330	335
Ser Ser Lys Leu Lys Arg His Gln Leu Val His Thr Gly Glu Lys Pro		
340	345	350
Phe Gln Cys Thr Phe Glu Gly Cys Gly Lys Arg Phe Ser Leu Asp Phe		

PH-1064PCT-US seq.TXT

355	360	365
Asn Leu Arg Thr His Val Arg Ile His Thr Gly Asp Arg Pro Tyr Val		
370	375	380
Cys Pro Phe Asp Gly Cys Asn Lys Lys Phe Ala Gln Ser Thr Asn Leu		
385	390	395
Lys Ser His Ile Leu Thr His Ala Lys Ala Lys Asn Asn Gln		400
405	410	

<210> 51

<211> 1229

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (222)..(950)

<400> 51

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ccaacattac ttgagtcttt ggataaaatt gagaaaagag tctacaagta ttgtggactc 180
tacaggaggc aggaggctga caactggcag taaagacaaa g atg tca ggc ctg cgg 236

Met Ser Gly Leu Arg

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ccc ggc act caa gtg gac cct gag att gag ctt ttt gta aag gct gga 284
Pro Gly Thr Gln Val Asp Pro Glu Ile Glu Leu Phe Val Lys Ala Gly

PH-1064PCT-US seq.TXT

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25	30	35	
atg atc ctc tgg ctt aaa gga gtt aaa ttt aat gtg aca act gtt gac	380		
Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn Val Thr Thr Val Asp			
40	45	50	
atg acc aga aag cct gaa gaa cta aag gac tta gcc cca ggt acc aat	428		
Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu Ala Pro Gly Thr Asn			
55	60	65	
cct ccg ttc ctg gtg tat aac aag gag ttg aaa aca gac ttc att aaa	476		
Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys Thr Asp Phe Ile Lys			
70	75	80	85
att gag gag ttt tta gaa caa acc ctg gct cct cca agg tac cct cac	524		
Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro Pro Arg Tyr Pro His			
90	95	100	
ctg agt ccc aag tac aag gag tct ttt gat gtg ggc tgt aac ctc ttt	572		
Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val Gly Cys Asn Leu Phe			
105	110	115	
gcc aag ttt tct gca tac att aag aat aca caa aag gag gca aat aag	620		
Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln Lys Glu Ala Asn Lys			
120	125	130	
aat ttt gaa aaa tct ctg ctc aaa gaa ttc aag cgt ctg gat gac tac	668		
Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys Arg Leu Asp Asp Tyr			

PH-1064PCT-US seq.TXT
140 145

135
tta aac acc cca ctt ctg gat gaa att gat cca gac agt gct ggg gaa 716
Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro Asp Ser Ala Gly Glu
150 155 160 165
ccc cca gtt tcc aga aga cta ttc ttg gat ggg gac cag cta aca ctg 764
Pro Pro Val Ser Arg Arg Leu Phe Leu Asp Gly Asp Gln Leu Thr Leu
170 175 180
gct gat tgt agc ttg tta ccc aag ctg aac att att aaa gtt gct gcc 812
Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile Ile Lys Val Ala Ala
185 190 195
aag aaa tat cgt gac ttt gac att cca gca gaa ttc tca gga gtc tgg 860
Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu Phe Ser Gly Val Trp
200 205 210
cgt tat ctc cac aat gcc tat gcc cgt gaa gaa ttt acc cac acg tgt 908
Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu Phe Thr His Thr Cys
215 220 225
cct gaa gac aaa gaa att gaa aat act tac gca aat gtg gct 950
Pro Glu Asp Lys Glu Ile Glu Asn Thr Tyr Ala Asn Val Ala
230 235 240
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<210> 52

<211> 243

<212> PRT

<213> Homo sapiens

<400> 52

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      20             25             30
Cys Gln Arg Leu Phe Met Ile Leu Trp Leu Lys Gly Val Lys Phe Asn
      35             40             45
Val Thr Thr Val Asp Met Thr Arg Lys Pro Glu Glu Leu Lys Asp Leu
      50             55             60
Ala Pro Gly Thr Asn Pro Pro Phe Leu Val Tyr Asn Lys Glu Leu Lys
      65             70             75             80
Thr Asp Phe Ile Lys Ile Glu Glu Phe Leu Glu Gln Thr Leu Ala Pro
      85             90             95
Pro Arg Tyr Pro His Leu Ser Pro Lys Tyr Lys Glu Ser Phe Asp Val
      100            105            110
Gly Cys Asn Leu Phe Ala Lys Phe Ser Ala Tyr Ile Lys Asn Thr Gln
      115            120            125
Lys Glu Ala Asn Lys Asn Phe Glu Lys Ser Leu Leu Lys Glu Phe Lys
      130            135            140
Arg Leu Asp Asp Tyr Leu Asn Thr Pro Leu Leu Asp Glu Ile Asp Pro

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PH-1064PCT-US seq.TXT

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	165	170	175
Asp Gln Leu Thr Leu Ala Asp Cys Ser Leu Leu Pro Lys Leu Asn Ile			
	180	185	190
Ile Lys Val Ala Ala Lys Lys Tyr Arg Asp Phe Asp Ile Pro Ala Glu			
	195	200	205
Phe Ser Gly Val Trp Arg Tyr Leu His Asn Ala Tyr Ala Arg Glu Glu			
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Asn Val Ala			

<210> 53

<211> 4001

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (2)..(316)

<400> 53

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PH-1064PCT-US seq.TXT

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Phe Asn Glu Ser Phe Ile Tyr Asp Ile Pro Thr Asp Leu Leu Pro Asp
      35              40              45
atc agc atc gag ttc ctc gtt atc gac ttc gat cgc acc acc aag aat 193
Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
      50              55              60
gag gtg gtg ggg agg ctg atc ctg ggg gca cac agt gtc aca gcc agt 241
Glu Val Val Gly Arg Leu Ile Leu Gly Ala His Ser Val Thr Ala Ser
      65              70              75              80
ggg gct gaa cac tgg aga gag gtc tgc gag agc ccc cgc aag cct gtg 289
Gly Ala Glu His Trp Arg Glu Val Cys Glu Ser Pro Arg Lys Pro Val
      85              90              95
gcc aag tgg cac agt ctg agc gag tac taatcctggt cttctctcct 336
Ala Lys Trp His Ser Leu Ser Glu Tyr
      100             105
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gactccaaac ctcatttttag ttgtagaaga aaattttctta caaaacaaat tccacaaaga 456
acaccctata tgaccacagc tgcagatcag ttcttagcaa tgatgttttt ttttctgctt 516
tgcaaggcgc tagaatcttt tattttactt tatttttttt gaggtggagt ttcgctcttg 576
ttgcccgggc tggagtgcaa tgggtgagatc tcaactcact gcaacctctg ccctccaggt 636
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PH-1064PCT-US seq.TXT

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<212> PRT

<213> Homo sapiens

<400> 54

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 35 40 45
 Ile Ser Ile Glu Phe Leu Val Ile Asp Phe Asp Arg Thr Thr Lys Asn
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65 70 75 80
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Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys
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Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr
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Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val
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ctc agc aca ctg tgt ctg gat gcc gcc tgc cca gac ctc ccc acc tac 645
Leu Ser Thr Leu Cys Leu Asp Ala Ala Cys Pro Asp Leu Pro Thr Tyr
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195

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210

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225

230

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<211> 264

<212> PRT

<213> Homo sapiens

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Ile Val Val Thr Asp Tyr Ser Asp Gln Asn Leu Gln Glu Leu Glu Lys			
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Trp Leu Lys Lys Glu Pro Glu Ala Phe Asp Trp Ser Pro Val Val Thr			
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Glu Lys Leu Arg Gln Ala Val Lys Gln Val Leu Lys Cys Asp Val Thr			
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Gln Ser Gln Pro Leu Gly Ala Val Pro Leu Pro Pro Ala Asp Cys Val			
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<210> 58

<211> 180

<212> PRT

<213> Homo sapiens

<400> 58

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Thr Ala Asp Ala Gln Leu Cys Asn His Gln Thr Cys Pro Met Lys Ala			
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agg agt cac atc tgt agc cac cca gga tgt ggc aag aca tac ttt aaa	1581				
Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr Tyr Phe Lys					
360		365		370	
agt tcc cat ctg aag gcc cac acg agg acg cac aca gga gaa aag cct	1629				
Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly Glu Lys Pro					
375		380		385	
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Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala Arg Ser Asp					
390		395		400	
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Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys Lys Phe Ala					
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Thr Gln

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cagaagcccc acagcctggc acgaaggccc cgtctggggtt aggtgactaa aagggttcg 2045
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<210> 60

<211> 469

<212> PRT

<213> Homo sapiens

<400> 60

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Asn	Leu	Leu	Pro	Gly	Thr	Pro	Asp	Phe	His	Thr	Ile	Pro	Ala	Phe	Cys
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 Ser Glu Thr Val Ile Cys Arg Ser Gln Pro Ala Pro Val Ser Pro Gln
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 Gln Lys Ser Val Leu Val Ser Pro Pro Ala Val Ser Ala Gly Gly Val
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Ser Arg Ile Arg Ser His Ile Cys Ser His Pro Gly Cys Gly Lys Thr
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Tyr Phe Lys Ser Ser His Leu Lys Ala His Thr Arg Thr His Thr Gly
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Glu Lys Pro Phe Ser Cys Ser Trp Lys Gly Cys Glu Arg Arg Phe Ala
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Arg Ser Asp Glu Leu Ser Arg His Arg Arg Thr His Thr Gly Glu Lys
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Lys Phe Ala Cys Pro Met Cys Asp Arg Arg Phe Met Arg Ser Asp His
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Leu Thr Lys His Ala Arg Arg His Leu Ser Ala Lys Lys Leu Pro Asn
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<210> 61

<211> 1428

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (125)..(868)

<400> 61

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Cys Arg Ile Tyr Val Gly Asn Leu Pro Pro Asp Ile Arg Thr Lys Asp
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Lys Asn Arg Arg Gly Gly Pro Pro Phe Ala Phe Val Glu Phe Glu Asp
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Tyr	Gly	Pro	Pro	Ser	Arg	Arg	Ser	Glu	Asn	Arg	Val	Val	Val	Ser	Gly		
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Asp	Asn	Thr	Lys	Phe	Arg	Ser	His	Glu	Gly	Glu	Thr	Ala	Tyr	Ile	Arg		
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195

200

205

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210

215

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225

230

235

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Arg His Ser Arg Ser Arg Ser Arg Thr

240

245

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65				70					75					80	
Gly	Tyr	Arg	Leu	Arg	Val	Glu	Phe	Pro	Arg	Ser	Gly	Arg	Gly	Thr	Gly
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Arg	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Ala	Pro	Arg	Gly	Arg	Tyr
		100						105					110		
Gly	Pro	Pro	Ser	Arg	Arg	Ser	Glu	Asn	Arg	Val	Val	Val	Ser	Gly	Leu
		115						120					125		
Pro	Pro	Ser	Gly	Ser	Trp	Gln	Asp	Leu	Lys	Asp	His	Met	Arg	Glu	Ala
	130					135						140			
Gly	Asp	Val	Cys	Tyr	Ala	Asp	Val	Tyr	Arg	Asp	Gly	Thr	Gly	Val	Val
145				150					155					160	
Glu	Phe	Val	Arg	Lys	Glu	Asp	Met	Thr	Tyr	Ala	Val	Arg	Lys	Leu	Asp
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<210> 63

<211> 3664

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (195)..(1943)

<400> 63

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Thr Pro Pro Glu Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro	
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Ile Leu Pro Pro Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser	
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Phe Phe Pro Arg Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly	
65 70 75	
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Gly Ile Asp Gly Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu	
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Gln Asp Met Asn Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val	
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ctc cag tca atg cgt gcc ctg gac ttc aac acc cgg act cag gtc acc	758
Leu Gln Ser Met Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr	
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Arg Glu Ala Ile Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly	
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Ala Thr Arg Arg Arg Lys Pro Cys Ser Arg Pro Leu Ser Ser Ile Leu	
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Gly Arg Ser Asn Leu Lys Phe Ala Gly Met Pro Ile Thr Leu Thr Val	
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Arg Ala Cys His Ile Leu Glu Cys Pro Glu Gly Leu Ala Gln Asp Val	
285 290 295 300	
atc agc acc att ggc cag gcc ttc gag ttg cgc ttc aaa caa tac ctc	1142
Ile Ser Thr Ile Gly Gln Ala Phe Glu Leu Arg Phe Lys Gln Tyr Leu	
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agg aac cca ccc aaa ctg gtc acc cct cat gac agg atg gct ggc ttt	1190
Arg Asn Pro Pro Lys Leu Val Thr Pro His Asp Arg Met Ala Gly Phe	
320 325 330	
gat ggc tca gca tgg gat gag gag gag gaa gag cca cct gac cat cag	1238
Asp Gly Ser Ala Trp Asp Glu Glu Glu Glu Glu Pro Pro Asp His Gln	
335 340 345	
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 agcctaggcc cggggtggcc acaccacagc aagccggccc cccctctttt ggcttgtgg 3343
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 aaaaaaaaaa tacatttata catcaccttt ttgacttttc caagcccttt tacagctctt 3523
 ggcattttcc tcgcctaggc ctgtgaggta actgggatcg caccttttat accagagacc 3583
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<211> 583

<212> PRT

<213> Homo sapiens

<400> 64

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Glu Leu Pro Ser Pro Ser Ala Ser Ser Leu Gly Pro Ile Leu Pro Pro
35 40 45
Leu Pro Gly Asp Asp Ser Pro Thr Thr Leu Cys Ser Phe Phe Pro Arg
50 55 60
Met Ser Asn Leu Arg Leu Ala Asn Pro Ala Gly Gly Arg Pro Gly Ser
65 70 75 80
Lys Gly Glu Pro Gly Arg Ala Ala Asp Asp Gly Glu Gly Ile Asp Gly
85 90 95
Ala Ala Met Pro Glu Ser Gly Pro Leu Pro Leu Leu Gln Asp Met Asn
100 105 110
Lys Leu Ser Gly Gly Gly Gly Arg Arg Thr Arg Val Glu Gly Gly Gln
115 120 125
Leu Gly Gly Glu Glu Trp Thr Arg His Gly Ser Phe Val Asn Lys Pro
130 135 140
Thr Arg Gly Trp Leu His Pro Asn Asp Lys Val Met Gly Pro Gly Val
145 150 155 160
Ser Tyr Leu Val Arg Tyr Met Gly Cys Val Glu Val Leu Gln Ser Met
165 170 175
Arg Ala Leu Asp Phe Asn Thr Arg Thr Gln Val Thr Arg Glu Ala Ile
180 185 190
Ser Leu Val Cys Glu Ala Val Pro Gly Ala Lys Gly Ala Thr Arg Arg
195 200 205

PH-1064PCT-US seq.TXT

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Tyr	Val	Ala	Tyr	Val	Ala	Lys	Asp	Pro	Val	Asn	Gln	Arg	Ala	Cys	His
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305						310					315				320
Lys	Leu	Val	Thr	Pro	His	Asp	Arg	Met	Ala	Gly	Phe	Asp	Gly	Ser	Ala
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Trp	Asp	Glu	Glu	Glu	Glu	Glu	Pro	Pro	Asp	His	Gln	Tyr	Tyr	Asn	Asp
						340					345				350
Phe	Pro	Gly	Lys	Glu	Pro	Pro	Leu	Gly	Gly	Val	Val	Asp	Met	Arg	Leu
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Arg	Glu	Gly	Ala	Ala	Pro	Gly	Ala	Ala	Arg	Pro	Thr	Ala	Pro	Asn	Ala
			370						375						380
Gln	Thr	Pro	Ser	His	Leu	Gly	Ala	Thr	Leu	Pro	Val	Gly	Gln	Pro	Val
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PH-1064PCT-US seq.TXT

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				420					425						430
Leu	Asp	Lys	Ala	Arg	Gln	Ala	Val	Gly	Gly	Ala	Gly	Pro	Pro	Asn	Pro
				435					440						445
Ala	Ile	Asn	Gly	Ser	Ala	Pro	Arg	Asp	Leu	Phe	Asp	Met	Lys	Pro	Phe
				450					455						460
Glu	Asp	Ala	Leu	Arg	Val	Pro	Pro	Pro	Pro	Gln	Ser	Val	Ser	Met	Ala
				465											480
Glu	Gln	Leu	Arg	Gly	Glu	Pro	Trp	Phe	His	Gly	Lys	Leu	Ser	Arg	Arg
				485											495
Glu	Ala	Glu	Ala	Leu	Leu	Gln	Leu	Asn	Gly	Asp	Phe	Leu	Val	Arg	Glu
				500											510
Ser	Thr	Thr	Thr	Pro	Gly	Gln	Tyr	Val	Leu	Thr	Gly	Leu	Gln	Ser	Gly
				515											525
Gln	Pro	Lys	His	Leu	Leu	Leu	Val	Asp	Pro	Glu	Gly	Val	Val	Arg	Thr
				530											540
Lys	Asp	His	Arg	Phe	Glu	Ser	Val	Ser	His	Leu	Ile	Ser	Tyr	His	Met
				545											560
Asp	Asn	His	Leu	Pro	Ile	Ile	Ser	Ala	Gly	Ser	Glu	Leu	Cys	Leu	Gln
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<210> 65

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<212> DNA

<213> Homo sapiens

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<222> (41)..(1237)

<400> 65

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Leu Gly Leu Val Val Cys Leu Val Leu Trp Pro Leu His Ser Glu Gly
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tct gga ggg aaa ctg aca gct gtg gat cct gaa aca aac atg aat gtg      151
Ser Gly Gly Lys Leu Thr Ala Val Asp Pro Glu Thr Asn Met Asn Val
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agt gaa att atc tct tac tgg gga ttc cct agt gag gaa tac cta gtt      199
Ser Glu Ile Ile Ser Tyr Trp Gly Phe Pro Ser Glu Glu Tyr Leu Val
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gag aca gaa gat gga tat att ctg tgc ctt aac cga att cct cat ggg      247
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70 75 80 85	
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His Gly Leu Leu Ala Asp Ser Ser Asn Trp Val Thr Asn Leu Ala Asn	
90 95 100	
agc agc ctg ggc ttc att ctt gct gat gct ggt ttt gac gtg tgg atg	391
Ser Ser Leu Gly Phe Ile Leu Ala Asp Ala Gly Phe Asp Val Trp Met	
105 110 115	
ggc aac agc aga gga aat acc tgg tct cgg aaa cat aag aca ctc tca	439
Gly Asn Ser Arg Gly Asn Thr Trp Ser Arg Lys His Lys Thr Leu Ser	
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gtt tct cag gat gaa ttc tgg gct ttc agt tat gat gag atg gca aaa	487
Val Ser Gln Asp Glu Phe Trp Ala Phe Ser Tyr Asp Glu Met Ala Lys	
135 140 145	
tat gac cta cca gct tcc att aac ttc att ctg aat aaa act ggc caa	535
Tyr Asp Leu Pro Ala Ser Ile Asn Phe Ile Leu Asn Lys Thr Gly Gln	
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gaa caa gtg tat tat gtg ggt cat tct caa ggc acc act ata ggt ttt	583
Glu Gln Val Tyr Tyr Val Gly His Ser Gln Gly Thr Thr Ile Gly Phe	
170 175 180	
ata gca ttt tca cag atc cct gag ctg gct aaa agg att aaa atg ttt	631
Ile Ala Phe Ser Gln Ile Pro Glu Leu Ala Lys Arg Ile Lys Met Phe	
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PH-1064PCT-US seq.TXT

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gcc aaa tta gga cga tta cca gat cat ctc att aag gac tta ttt gga 727
Ala Lys Leu Gly Arg Leu Pro Asp His Leu Ile Lys Asp Leu Phe Gly
      215                      220                      225

gac aaa gaa ttt ctt ccc cag agt gcg ttt ttg aag tgg ctg ggt acc 775
Asp Lys Glu Phe Leu Pro Gln Ser Ala Phe Leu Lys Trp Leu Gly Thr
230                      235                      240                      245

cac gtt tgc act cat gtc ata ctg aag gag ctc tgt gga aat ctc tgt 823
His Val Cys Thr His Val Ile Leu Lys Glu Leu Cys Gly Asn Leu Cys
      250                      255                      260

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Phe Leu Leu Cys Gly Phe Asn Glu Arg Asn Leu Asn Met Ser Arg Val
      265                      270                      275

gat gta tat aca aca cat tct cct gct gga act tct gtg caa aac atg 919
Asp Val Tyr Thr Thr His Ser Pro Ala Gly Thr Ser Val Gln Asn Met
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tta cac tgg agc cag gct gtt aaa ttc caa aag ttt caa gcc ttt gac 967
Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys Phe Gln Ala Phe Asp
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ggg ggt cac gac tgg ctt gca gat gtc tac gac gtc aat atc tta ctg 1111
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          345                      350                      355

act cag atc acc aac ttg gtg ttc cat gag agc att ccg gaa tgg gag 1159
Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser Ile Pro Glu Trp Glu
          360                      365                      370

cat ctt gac ttc att tgg ggc ctg gat gcc cct tgg agg ctt tat aat 1207
His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro Trp Arg Leu Tyr Asn
          375                      380                      385

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Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln
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<211> 399

<212> PRT

<213> Homo sapiens

<400> 66

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					20				25					30	
Thr	Asn	Met	Asn	Val	Ser	Glu	Ile	Ile	Ser	Tyr	Trp	Gly	Phe	Pro	Ser
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PH-1064PCT-US seq.TXT

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				85					90					95	
Thr	Asn	Leu	Ala	Asn	Ser	Ser	Leu	Gly	Phe	Ile	Leu	Ala	Asp	Ala	Gly
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Phe	Asp	Val	Trp	Met	Gly	Asn	Ser	Arg	Gly	Asn	Thr	Trp	Ser	Arg	Lys
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His	Lys	Thr	Leu	Ser	Val	Ser	Gln	Asp	Glu	Phe	Trp	Ala	Phe	Ser	Tyr
	130					135					140				
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Thr	Thr	Ile	Gly	Phe	Ile	Ala	Phe	Ser	Gln	Ile	Pro	Glu	Leu	Ala	Lys
		180						185				190			
Arg	Ile	Lys	Met	Phe	Phe	Ala	Leu	Gly	Pro	Val	Ala	Ser	Val	Ala	Phe
		195					200					205			
Cys	Thr	Ser	Pro	Met	Ala	Lys	Leu	Gly	Arg	Leu	Pro	Asp	His	Leu	Ile
	210					215					220				
Lys	Asp	Leu	Phe	Gly	Asp	Lys	Glu	Phe	Leu	Pro	Gln	Ser	Ala	Phe	Leu
225					230				235					240	
Lys	Trp	Leu	Gly	Thr	His	Val	Cys	Thr	His	Val	Ile	Leu	Lys	Glu	Leu

PH-1064PCT-US seq.TXT

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275	280	285
Ser Val Gln Asn Met Leu His Trp Ser Gln Ala Val Lys Phe Gln Lys		
290	295	300
Phe Gln Ala Phe Asp Trp Gly Ser Ser Ala Lys Asn Tyr Phe His Tyr		
305	310	315
Asn Gln Ser Tyr Pro Pro Thr Tyr Asn Val Lys Asp Met Leu Val Pro		
325	330	335
Thr Ala Val Trp Ser Gly Gly His Asp Trp Leu Ala Asp Val Tyr Asp		
340	345	350
Val Asn Ile Leu Leu Thr Gln Ile Thr Asn Leu Val Phe His Glu Ser		
355	360	365
Ile Pro Glu Trp Glu His Leu Asp Phe Ile Trp Gly Leu Asp Ala Pro		
370	375	380
Trp Arg Leu Tyr Asn Lys Ile Ile Asn Leu Met Arg Lys Tyr Gln		
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<400> 67

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agcagcagac aggattccag gaaccagtgt ttgatgaagc taggactgag gagcaagcga 180
gcaagcagca gttcgtggaa tcctgtctgc tgctgtcttc ctggtttagg agccgacggg 240
cgctcgcagg ctccgcgcgc gctgccgcgc gcaggacccg gccgcctccg ccgccgcgcgc 300
cgccccctaag cctcccgaag cc atg gcc ggg ctc ggc cac ccc gcc gcc ttc 352

Met Ala Gly Leu Gly His Pro Ala Ala Phe

1 5 10

ggc cgg gcc acc cac gcc gtg gtg cgg gcg cta ccc gag tcg ctc ggc 400

Gly Arg Ala Thr His Ala Val Val Arg Ala Leu Pro Glu Ser Leu Gly

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Gln His Ala Leu Arg Ser Ala Lys Gly Glu Glu Val Asp Val Ala Arg

30 35 40

gcg gaa cgg cag cac cag ctc tac gtg ggc gtg ctg ggc agc aag ctg 496

Ala Glu Arg Gln His Gln Leu Tyr Val Gly Val Leu Gly Ser Lys Leu

45 50 55

ggg ctg cag gtg gtg gag ctg ccg gcc gac gag agc ctt ccg gac tgc 544

Gly Leu Gln Val Val Glu Leu Pro Ala Asp Glu Ser Leu Pro Asp Cys

60 65 70

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  75                      80                      85                      90
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Thr Arg Pro Gly Ala Pro Ser Arg Arg Lys Glu Val Asp Met Met Lys
                      95                      100                      105
gaa gca tta gaa aaa ctt cag ctc aat ata gta gag atg aaa gat gaa      688
Glu Ala Leu Glu Lys Leu Gln Leu Asn Ile Val Glu Met Lys Asp Glu
                      110                      115                      120
aat gca act tta gat ggc gga gat gtt tta ttc aca ggc aga gaa ttt      736
Asn Ala Thr Leu Asp Gly Gly Asp Val Leu Phe Thr Gly Arg Glu Phe
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Phe Val Gly Leu Ser Lys Arg Thr Asn Gln Arg Gly Ala Glu Ile Leu
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gct gat act ttt aag gac tat gca gtc tcc aca gtg cca gtg gca gat      832
Ala Asp Thr Phe Lys Asp Tyr Ala Val Ser Thr Val Pro Val Ala Asp
155                      160                      165                      170
ggg ttg cat ttg aag agt ttc tgc agc atg gct ggg cct aac ctg atc      880
Gly Leu His Leu Lys Ser Phe Cys Ser Met Ala Gly Pro Asn Leu Ile
                      175                      180                      185
gca att ggg tct agt gaa tct gca cag aag gcc ctt aag atc atg caa      928
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205

210

215

gca gca aac tgt ata tat cta aat atc ccc aac aaa ggg cac gtc ttg 1024

Ala Ala Asn Cys Ile Tyr Leu Asn Ile Pro Asn Lys Gly His Val Leu

220

225

230

ctg cac cga acc ccg gaa gag tat cca gaa agt gca aag gtt tat gag 1072

Leu His Arg Thr Pro Glu Glu Tyr Pro Glu Ser Ala Lys Val Tyr Glu

235

240

245

250

aaa ctg aag gac cat atg ctg atc ccc gtg agc atg tct gaa ctg gaa 1120

Lys Leu Lys Asp His Met Leu Ile Pro Val Ser Met Ser Glu Leu Glu

255

260

265

aag gtg gat ggg ctg ctc acc tgc tgc tca gtt tta att aac aag aaa 1168

Lys Val Asp Gly Leu Leu Thr Cys Cys Ser Val Leu Ile Asn Lys Lys

270

275

280

gta gac tcc tgagctgcag agtccccccc ggtagccggc aagaccgcac 1217

Val Asp Ser

285

aggcaaggcc gatgactctg tgcccactcc tgttggttttc cttgacaatc tactgtgcca 1277

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<211> 285

<212> PRT

<213> Homo sapiens

<400> 68

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 35 40 45
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 50 55 60
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 65 70 75 80
 Ala Val Val Cys Glu Glu Thr Ala Leu Ile Thr Arg Pro Gly Ala Pro
 85 90 95
 Ser Arg Arg Lys Glu Val Asp Met Met Lys Glu Ala Leu Glu Lys Leu
 100 105 110
 Gln Leu Asn Ile Val Glu Met Lys Asp Glu Asn Ala Thr Leu Asp Gly
 115 120 125
 Gly Asp Val Leu Phe Thr Gly Arg Glu Phe Phe Val Gly Leu Ser Lys
 130 135 140

PH-1064PCT-US seq.TXT

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Phe	Cys	Ser	Met	Ala	Gly	Pro	Asn	Leu	Ile	Ala	Ile	Gly	Ser	Ser	Glu
			180					185						190	
Ser	Ala	Gln	Lys	Ala	Leu	Lys	Ile	Met	Gln	Gln	Met	Ser	Asp	His	Arg
		195					200					205			
Tyr	Asp	Lys	Leu	Thr	Val	Pro	Asp	Asp	Ile	Ala	Ala	Asn	Cys	Ile	Tyr
	210					215						220			
Leu	Asn	Ile	Pro	Asn	Lys	Gly	His	Val	Leu	Leu	His	Arg	Thr	Pro	Glu
225				230					235						240
Glu	Tyr	Pro	Glu	Ser	Ala	Lys	Val	Tyr	Glu	Lys	Leu	Lys	Asp	His	Met
				245					250					255	
Leu	Ile	Pro	Val	Ser	Met	Ser	Glu	Leu	Glu	Lys	Val	Asp	Gly	Leu	Leu
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gaaagaacgt tcccacctgc ctagcc atg gga gag gac gct gca cag gcc gaa 173

Met Gly Glu Asp Ala Ala Gln Ala Glu

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ccc agc ccg atg cct tcc tcc aca cca agc ccc agc ctg aac cta ggg 269
Pro Ser Pro Met Pro Ser Ser Thr Pro Ser Pro Ser Leu Asn Leu Gly
30 35 40

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Asn Thr Glu Glu Ala Ile Arg Asp Asn Ser Gln Val Asn Ala Val Thr
45 50 55

gtg ctc acg ctc ctg gac aag ctg gtg aac atg cta gac gct gtg cag 365
Val Leu Thr Leu Leu Asp Lys Leu Val Asn Met Leu Asp Ala Val Gln
60 65 70

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Glu Asn Gln His Lys Met Glu Gln Arg Gln Ile Ser Leu Glu Gly Ser
75 80 85

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PH-1064PCT-US seq.TXT

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Ser	Thr	Ser	Asn	Thr	Val	Ser	Lys	Leu	Leu	Glu	Lys	Ser	Arg	Lys	Val		
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agc	gcc	cac	acg	cgc	gcg	gtc	aaa	gag	cgc	atg	gat	agg	cag	tgc	gca	557	
Ser	Ala	His	Thr	Arg	Ala	Val	Lys	Glu	Arg	Met	Asp	Arg	Gln	Cys	Ala		
			125					130					135				
cag	gtg	aag	cgg	ctg	gag	aac	aac	cac	gcc	cag	ctc	ctc	cga	cgc	aac	605	
Gln	Val	Lys	Arg	Leu	Glu	Asn	Asn	His	Ala	Gln	Leu	Leu	Arg	Arg	Asn		
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cat	ttc	aaa	gtg	ctc	atc	ttc	cag	gag	gaa	aat	gag	atc	cct	gcc	agc	653	
His	Phe	Lys	Val	Leu	Ile	Phe	Gln	Glu	Glu	Asn	Glu	Ile	Pro	Ala	Ser		
	155					160				165							
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Leu	Ser	Ser	Asp	Asp	Asp	Leu	Pro	His	Asp	Glu	Glu	Ala	Leu	Glu	Asp		
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PH-1064PCT-US seq.TXT

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235 240 245
aac atc gag aaa aag atg aac aag ctg ggg aca aag atc gta tct gta 941
Asn Ile Glu Lys Lys Met Asn Lys Leu Gly Thr Lys Ile Val Ser Val
250 255 260 265
gag agg aga gag aag att aag aaa tct ctc acg tca aat cac cag aaa 989
Glu Arg Arg Glu Lys Ile Lys Lys Ser Leu Thr Ser Asn His Gln Lys
270 275 280
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Ile Ser Ser Gly Lys Ser Ser Pro Phe Lys Val Ser Pro Leu Thr Phe
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Gly Arg Lys Lys Val Arg Glu Gly Glu Ser His Ala Glu Asn Glu Thr
300 305 310
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Lys Ser Glu Asp Leu Pro Ser Ser Glu Gln Met Pro Asn Asp Gln Glu
315 320 325
gag gag tcc ttt gca gag ggt cat tcc gaa gcg tcc ctc gcc agc gct 1181
Glu Glu Ser Phe Ala Glu Gly His Ser Glu Ala Ser Leu Ala Ser Ala
330 335 340 345
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PH-1064PCT-US seq.TXT

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365 370 375
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Glu Asp Glu Glu Glu Glu Ser Val Ala Leu Glu Gln Ala Gln Lys Val
380 385 390
cgc tat gag ggt agc tac gcg cta aca tcc gag gag gcg gag cgc tcc 1373
Arg Tyr Glu Gly Ser Tyr Ala Leu Thr Ser Glu Glu Ala Glu Arg Ser
395 400 405
gat ggg gac ccc gtg cag ccc gcc gtg ctc cag gtg cac cag acc tcc 1421
Asp Gly Asp Pro Val Gln Pro Ala Val Leu Gln Val His Gln Thr Ser
410 415 420 425
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<212> PRT

<213> Homo sapiens

PH-1064PCT-US seq.TXT

<400> 70

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			20					25					30		
Thr	Pro	Ser	Pro	Ser	Leu	Asn	Leu	Gly	Asn	Thr	Glu	Glu	Ala	Ile	Arg
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Lys	Leu	Leu	Glu	Lys	Ser	Arg	Lys	Val	Ser	Ala	His	Thr	Arg	Ala	Val
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145					150					155				160	
Gln	Glu	Glu	Asn	Glu	Ile	Pro	Ala	Ser	Val	Phe	Val	Lys	Gln	Pro	Val
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PH-1064PCT-US seq.TXT

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225	230	235
Ser Leu Lys Lys Ala Phe Ser Arg Gln Asn Ile Glu Lys Lys Met Asn		
245	250	255
Lys Leu Gly Thr Lys Ile Val Ser Val Glu Arg Arg Glu Lys Ile Lys		
260	265	270
Lys Ser Leu Thr Ser Asn His Gln Lys Ile Ser Ser Gly Lys Ser Ser		
275	280	285
Pro Phe Lys Val Ser Pro Leu Thr Phe Gly Arg Lys Lys Val Arg Glu		
290	295	300
Gly Glu Ser His Ala Glu Asn Glu Thr Lys Ser Glu Asp Leu Pro Ser		
305	310	315
Ser Glu Gln Met Pro Asn Asp Gln Glu Glu Glu Ser Phe Ala Glu Gly		
325	330	335
His Ser Glu Ala Ser Leu Ala Ser Ala Leu Val Glu Gly Glu Ile Ala		
340	345	350
Glu Glu Ala Ala Glu Lys Ala Thr Ser Arg Gly Ser Asn Ser Gly Met		
355	360	365
Asp Ser Asn Ile Asp Leu Thr Ile Val Glu Asp Glu Glu Glu Glu Ser		

PH-1064PCT-US seq.TXT

370	375	380
Val Ala Leu Glu Gln Ala Gln Lys Val Arg Tyr Glu Gly Ser Tyr Ala		
385	390	395
Leu Thr Ser Glu Glu Ala Glu Arg Ser Asp Gly Asp Pro Val Gln Pro		
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<211> 2638

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (288)..(1844)

<400> 71

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 cactgactcc cagctgtggg cttcaccatt acagactccc cagggcttca aagacttctc 240
 agcttcgagc atggcttttg gctgtcaggg cagctgtaca atagtgg atg ttt gag 296

Met Phe Glu

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acg gag gca gat gag aag agg gag atg gcc ttg gag gaa ggg aag ggg 344

PH-1064PCT-US seq.TXT

Thr	Glu	Ala	Asp	Glu	Lys	Arg	Glu	Met	Ala	Leu	Glu	Glu	Gly	Lys	Gly		
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Pro	Gly	Ala	Glu	Asp	Ser	Pro	Pro	Ser	Lys	Glu	Pro	Ser	Pro	Gly	Gln		
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Glu	Leu	Pro	Pro	Gly	Gln	Asp	Leu	Pro	Pro	Asn	Lys	Asp	Ser	Pro	Ser		
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Gly	Gln	Glu	Pro	Ala	Pro	Ser	Gln	Glu	Pro	Leu	Ser	Ser	Lys	Asp	Ser		
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Ala	Thr	Ser	Glu	Gly	Ser	Pro	Pro	Gly	Pro	Asp	Ala	Pro	Pro	Ser	Lys		
				70						75				80			
gat	gtg	cca	cca	tgc	cag	gaa	ccc	cct	cca	gcc	caa	gac	ctc	tca	ccc	584	
Asp	Val	Pro	Pro	Cys	Gln	Glu	Pro	Pro	Pro	Ala	Gln	Asp	Leu	Ser	Pro		
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tgc	cag	gac	cta	cct	gct	ggt	caa	gaa	ccc	ctg	cct	cac	cag	gac	cct	632	
Cys	Gln	Asp	Leu	Pro	Ala	Gly	Gln	Glu	Pro	Leu	Pro	His	Gln	Asp	Pro		
100					105					110				115			
cta	ctc	acc	aaa	gac	ctc	cct	gcc	atc	cag	gaa	tcc	ccc	acc	cg	gac	680	
Leu	Leu	Thr	Lys	Asp	Leu	Pro	Ala	Ile	Gln	Glu	Ser	Pro	Thr	Arg	Asp		
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Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu Leu Ala Ala
      150              155              160
act ggg gac cca cct gcg gcc ccc agg cca gcc ttc gtg atc cct gag 824
Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val Ile Pro Glu
      165              170              175
gtc cgg ctg gat agc acc tac agc cag aag gca ggg gca gag cag ggc 872
Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala Glu Gln Gly
      180              185              190              195
tgc tcg gga gat gag gag gat gca gaa gag gcc gag gag gtg gag gag 920
Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu Val Glu Glu
      200              205              210
ggg gag gaa ggg gag gag gac gag gat gag gac acc agc gat gac aac 968
Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser Asp Asp Asn
      215              220              225
tac gga gag cgc agt gag gcc aag cgc agc agc atg atc gag acg ggc 1016
Tyr Gly Glu Arg Ser Glu Ala Lys Arg Ser Ser Met Ile Glu Thr Gly
      230              235              240
cag ggg gct gag ggt ggc ctc tca ctg cgt gtg cag aac tcg ctg cgg 1064
Gln Gly Ala Glu Gly Gly Leu Ser Leu Arg Val Gln Asn Ser Leu Arg
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Cys	Phe	Ala	Ser	Asp	Thr	Thr	Leu	His	Cys	Ser	Asp	Gly	Glu	Gly	Ala		
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gcc	tcc	acc	tgg	ggc	atg	cct	tcg	ccc	agc	acc	ctc	aag	aaa	gag	ctg	1208	
Ala	Ser	Thr	Trp	Gly	Met	Pro	Ser	Pro	Ser	Thr	Leu	Lys	Lys	Glu	Leu		
				295					300					305			
ggc	cgc	aat	ggt	ggc	tcc	atg	cac	cac	ctt	tcc	ctc	ttc	ttc	aca	gga	1256	
Gly	Arg	Asn	Gly	Gly	Ser	Met	His	His	Leu	Ser	Leu	Phe	Phe	Thr	Gly		
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cac	agg	aag	atg	agc	ggg	gct	gac	acc	gtt	ggg	gat	gat	gac	gaa	gcc	1304	
His	Arg	Lys	Met	Ser	Gly	Ala	Asp	Thr	Val	Gly	Asp	Asp	Asp	Glu	Ala		
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Ser	Arg	Lys	Arg	Lys	Ser	Lys	Asn	Leu	Ala	Lys	Asp	Met	Lys	Asn	Lys		
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ctg	ggg	atc	ttc	aga	cgg	cgg	aat	gag	tcc	cct	gga	gcc	cct	ccc	gcg	1400	
Leu	Gly	Ile	Phe	Arg	Arg	Arg	Asn	Glu	Ser	Pro	Gly	Ala	Pro	Pro	Ala		
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ggc	aag	gca	gac	aaa	atg	atg	aag	tca	ttc	aag	ccc	acc	tca	gag	gaa	1448	
Gly	Lys	Ala	Asp	Lys	Met	Met	Lys	Ser	Phe	Lys	Pro	Thr	Ser	Glu	Glu		
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Gly	Leu	Ala	Val	Phe	Gln	Ala	Phe	Leu	Arg	Thr	Glu	Phe	Ser	Glu	Glu	
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aat	ctg	gag	ttc	tgg	ttg	gct	tgt	gag	gac	ttc	aag	aag	gtc	aag	tca	1592
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Gln	Ser	Lys	Met	Ala	Ser	Lys	Ala	Lys	Lys	Ile	Phe	Ala	Glu	Tyr	Ile	
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Ala	Ile	Gln	Ala	Cys	Lys	Glu	Val	Asn	Leu	Asp	Ser	Tyr	Thr	Arg	Glu	
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His	Thr	Lys	Asp	Asn	Leu	Gln	Ser	Val	Thr	Arg	Gly	Cys	Phe	Asp	Leu	
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Phe	Leu	Arg	Ser	Asp	Leu	Tyr	Leu	Asp	Leu	Ile	Asn	Gln	Lys	Lys	Met	
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Ser Pro Pro Leu

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<212> PRT

<213> Homo sapiens

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65	70	75
Pro Ser Lys Asp Val Pro Pro Cys Gln Glu Pro Pro Pro Ala Gln Asp		
85	90	95
Leu Ser Pro Cys Gln Asp Leu Pro Ala Gly Gln Glu Pro Leu Pro His		
100	105	110
Gln Asp Pro Leu Leu Thr Lys Asp Leu Pro Ala Ile Gln Glu Ser Pro		
115	120	125
Thr Arg Asp Leu Pro Pro Cys Gln Asp Leu Pro Pro Ser Gln Val Ser		
130	135	140
Leu Pro Ala Lys Ala Leu Thr Glu Asp Thr Met Ser Ser Gly Asp Leu		
145	150	155
Leu Ala Ala Thr Gly Asp Pro Pro Ala Ala Pro Arg Pro Ala Phe Val		
165	170	175
Ile Pro Glu Val Arg Leu Asp Ser Thr Tyr Ser Gln Lys Ala Gly Ala		
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Glu Gln Gly Cys Ser Gly Asp Glu Glu Asp Ala Glu Glu Ala Glu Glu		
195	200	205
Val Glu Glu Gly Glu Glu Gly Glu Glu Asp Glu Asp Glu Asp Thr Ser		
210	215	220
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PH-1064PCT-US seq.TXT

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Ser Leu Arg Arg Arg Thr His Ser Glu Gly Ser Leu Leu Gln Glu Pro			
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Arg Gly Pro Cys Phe Ala Ser Asp Thr Thr Leu His Cys Ser Asp Gly			
	275	280	285
Glu Gly Ala Ala Ser Thr Trp Gly Met Pro Ser Pro Ser Thr Leu Lys			
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Lys Glu Leu Gly Arg Asn Gly Gly Ser Met His His Leu Ser Leu Phe			
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Phe Thr Gly His Arg Lys Met Ser Gly Ala Asp Thr Val Gly Asp Asp			
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Asp Glu Ala Ser Arg Lys Arg Lys Ser Lys Asn Leu Ala Lys Asp Met			
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Lys Asn Lys Leu Gly Ile Phe Arg Arg Arg Asn Glu Ser Pro Gly Ala			
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Pro Pro Ala Gly Lys Ala Asp Lys Met Met Lys Ser Phe Lys Pro Thr			
	370	375	380
Ser Glu Glu Ala Leu Lys Trp Gly Glu Ser Leu Glu Lys Leu Leu Val			
385	390	395	400
His Lys Tyr Gly Leu Ala Val Phe Gln Ala Phe Leu Arg Thr Glu Phe			
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          465              470              475              480
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          485              490              495
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<212> DNA

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<222> (250)..(1206)

<400> 73

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 Gly Glu Tyr Glu Ala Ala Val Thr Leu Glu Lys Gln Glu Asp Leu Lys
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 Thr Leu Leu Ala His Pro Val Thr Leu Gly Glu Gln Gln Trp Lys Ser
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 Glu Lys Gln Arg Glu Ala Glu Leu Pro Lys Lys Lys Leu Glu Gln Arg
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 Ser Lys Leu Glu Asn Leu Glu Asp Leu Glu Ile Ile Ile Gln Leu Lys
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Glu Pro Glu Ile Ile Thr Glu Pro Val Asp Val Pro Thr Phe Leu Lys

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Leu Ile Met Tyr Gly Ala Asp Leu Asn Ile Lys Asn Cys Ala Gly Lys
275 280 285
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Thr Pro Met Asp Leu Val Leu His Trp Gln Asn Gly Thr Lys Ala Ile
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Phe Asp Ser Leu Arg Glu Asn Ser Tyr Lys Thr Ser Arg Ile Ala Thr
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<212> PRT

<213> Homo sapiens

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<400> 75

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Gln Asn Leu Leu Lys Ile Thr Asn Leu Arg Ile Lys Phe Val Lys Leu	
225	230 235 240
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Lys Tyr Tyr Tyr Ala Val Tyr Asp Met Val Val Arg Gly Asn Cys Phe	
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Cys Tyr Gly His Ala Ser Glu Cys Ala Pro Val Asp Gly Phe Asn Glu	
275	280 285
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Glu Val Glu Gly Met Val His Gly His Cys Met Cys Arg His Asn Thr	
290	295 300
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Lys Gly Leu Asn Cys Glu Leu Cys Met Asp Phe Tyr His Asp Leu Pro	
305	310 315 320
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Glu	Gly	Glu	His	Cys	Asp	Val	Cys	Lys	Glu	Gly	Phe	Tyr	Asp	Leu	Ser	
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Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
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980	985
990	
gag act ggg agg tgt ctc aag tgc ctg tac cac acg gaa ggg gaa cac	3141
Glu Thr Gly Arg Cys Leu Lys Cys Leu Tyr His Thr Glu Gly Glu His	
995	1000
1005	
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Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp	
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Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys	
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1055	
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Phe	Trp	Gly	Asp	Pro	Asp	Val	Glu	Cys	Arg	Ala	Cys	Asp	Cys	Asp	Pro		
			1125						1130					1135			
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		1140					1145						1150				
tgc	gtt	gag	ggt	gtt	gag	ggt	cca	cgc	tgt	gac	aag	tgc	acg	cga	ggg	3621	
Cys	Val	Glu	Gly	Val	Glu	Gly	Pro	Arg	Cys	Asp	Lys	Cys	Thr	Arg	Gly		
	1155					1160						1165					
tac	tcg	ggg	gtc	ttc	cct	gac	tgc	aca	ccc	tgc	cac	cag	tgc	ttt	gct	3669	
Tyr	Ser	Gly	Val	Phe	Pro	Asp	Cys	Thr	Pro	Cys	His	Gln	Cys	Phe	Ala		
1170					1175						1180						
ctc	tgg	gat	gtg	atc	att	gcc	gag	ctg	acc	aac	agg	aca	cac	aga	ttc	3717	
Leu	Trp	Asp	Val	Ile	Ile	Ala	Glu	Leu	Thr	Asn	Arg	Thr	His	Arg	Phe		
1185				1190						1195					1200		
ctg	gag	aaa	gcc	aag	gcc	ttg	aag	atc	agt	ggt	gtg	atc	ggg	cct	tac	3765	
Leu	Glu	Lys	Ala	Lys	Ala	Leu	Lys	Ile	Ser	Gly	Val	Ile	Gly	Pro	Tyr		
		1205							1210				1215				
cgt	gag	act	gtg	gac	tcg	gtg	gag	agg	aaa	gtc	agc	gag	ata	aaa	gac	3813	

PH-1064PCT-US seq.TXT

Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp

1220

1225

1230

atc ctg gcg cag agc ccc gca gca gag cca ctg aaa aac att ggg aat 3861

Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn

1235

1240

1245

ctc ttt gag gaa gca gag aaa ctg att aaa gat gtt aca gaa atg atg 3909

Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met

1250

1255

1260

gct caa gta gaa gtg aaa tta tct gac aca act tcc caa agc aac agc 3957

Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser

1265

1270

1275

1280

aca gcc aaa gaa ctg gat tct cta cag aca gaa gcc gaa agc cta gac 4005

Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp

1285

1290

1295

aac act gtg aaa gaa ctt gct gaa caa ctg gaa ttt atc aaa aac tca 4053

Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser

1300

1305

1310

gat att cgg ggt gcc ttg gat agc att acc aag tat ttc cag atg tct 4101

Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser

1315

1320

1325

ctt gag gca gag gag agg gtg aat gcc tcc acc aca gaa ccc aac agc 4149

Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser

1330

1335

1340

act gtg gag cag tca gcc ctc atg aga gac aga gta gaa gac gtg atg 4197

Thr	Val	Glu	Gln	Ser	Ala	Leu	Met	Arg	Asp	Arg	Val	Glu	Asp	Val	Met	
1345					1350				1355					1360		
atg	gag	cga	gaa	tcc	cag	ttc	aag	gaa	aaa	caa	gag	gag	cag	gct	cgc	4245
Met	Glu	Arg	Glu	Ser	Gln	Phe	Lys	Glu	Lys	Gln	Glu	Glu	Gln	Ala	Arg	
				1365				1370						1375		
ctc	ctt	gat	gaa	ctg	gca	ggc	aag	cta	caa	agc	cta	gac	ctt	tca	gcc	4293
Leu	Leu	Asp	Glu	Leu	Ala	Gly	Lys	Leu	Gln	Ser	Leu	Asp	Leu	Ser	Ala	
				1380				1385						1390		
gct	gcc	gaa	atg	acc	tgt	gga	aca	ccc	cca	ggg	gcc	tcc	tgt	tcc	gag	4341
Ala	Ala	Glu	Met	Thr	Cys	Gly	Thr	Pro	Pro	Gly	Ala	Ser	Cys	Ser	Glu	
				1395				1400						1405		
act	gaa	tgt	ggc	ggg	cca	aac	tgc	aga	act	gac	gaa	gga	gag	agg	aag	4389
Thr	Glu	Cys	Gly	Gly	Pro	Asn	Cys	Arg	Thr	Asp	Glu	Gly	Glu	Arg	Lys	
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tgt	ggg	ggg	cct	ggc	tgt	ggg	ggg	ctg	gtt	act	gtt	gca	cac	aac	gcc	4437
Cys	Gly	Gly	Pro	Gly	Cys	Gly	Gly	Leu	Val	Thr	Val	Ala	His	Asn	Ala	
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tgg	cag	aaa	gcc	atg	gac	ttg	gac	caa	gat	gtc	ctg	agt	gcc	ctg	gct	4485
Trp	Gln	Lys	Ala	Met	Asp	Leu	Asp	Gln	Asp	Val	Leu	Ser	Ala	Leu	Ala	
				1445				1450						1455		
gaa	gtg	gaa	cag	ctc	tcc	aag	atg	gtc	tct	gaa	gca	aaa	ctg	agg	gca	4533
Glu	Val	Glu	Gln	Leu	Ser	Lys	Met	Val	Ser	Glu	Ala	Lys	Leu	Arg	Ala	
				1460				1465						1470		
gat	gag	gca	aaa	caa	agt	gct	gaa	gac	att	ctg	ttg	aag	aca	aat	gct	4581

PH-1064PCT-US seq.TXT

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 acc aaa gaa aaa atg gac aag agc aat gag gag ctg aga aat cta atc 4629
 Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile
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 Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser
 1505 1510 1515 1520
 att gaa gca gtt gct aat gaa gta ttg aaa atg gag atg cct agc acc 4725
 Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr
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 cca cag cag tta cag aac ttg aca gaa gat ata cgt gaa cga gtt gaa 4773
 Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu
 1540 1545 1550
 agc ctt tct caa gta gag gtt att ctt cag cat agt gct gct gac att 4821
 Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile
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 gcc aga gct gag atg ttg tta gaa gaa gct aaa aga gca agc aaa agt 4869
 Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser
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 gca aca gat gtt aaa gtc act gca gat atg gta aag gaa gct ctg gaa 4917
 Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu
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PH-1064PCT-US seq.TXT

Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala	
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Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser	
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1630	
gaa aca gca gct tct gag gaa acc ttg ttc aac gcg tcc cag cgc atc	5061
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile	
1635	1640
1645	
agc gag tta gag agg aat gtg gaa gaa ctt aag cgg aaa gct gcc caa	5109
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln	
1650	1655
1660	
aac tcc ggg gag gca gaa tat att gaa aaa gta gta tat act gtg aag	5157
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys	
1665	1670
1675	1680
caa agt gca gaa gat gtt aag aag act tta gat ggt gaa ctt gat gaa	5205
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu	
1685	1690
1695	
aag tat aaa aaa gta gaa aat tta att gcc aaa aaa act gaa gag tca	5253
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser	
1700	1705
1710	
gct gat gcc aga agg aaa gcc gaa atg cta caa aat gaa gca aaa act	5301
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr	
1715	1720
1725	
ctt tta gct caa gca aat agc aag ctg caa ctg ctc aaa gat tta gaa	5349

PH-1064PCT-US seq.TXT

Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu
 1730 1735 1740
 aga aaa tat gaa gac aat caa aga tac tta gaa gat aaa gct caa gaa 5397
 Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu
 1745 1750 1755 1760
 tta gca aga ctg gaa gga gaa gtc cgt tca ctc cta aag gat ata agc 5445
 Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser
 1765 1770 1775
 cag aaa gtt gct gtg tat agc aca tgc ttg taacagagga gaataaaaaa 5495
 Gln Lys Val Ala Val Tyr Ser Thr Cys Leu
 1780 1785
 tggctgaggt gaacaaggta aaacaactac attttaaaaa ctgacttaat gctcttcaaa 5555
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<210> 76

<211> 1786

<212> PRT

<213> Homo sapiens

<400> 76

Met Gly Leu Leu Gln Leu Leu Ala Phe Ser Phe Leu Ala Leu Cys Arg
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 Ala Arg Val Arg Ala Gln Glu Pro Glu Phe Ser Tyr Gly Cys Ala Glu
 20 25 30
 Gly Ser Cys Tyr Pro Ala Thr Gly Asp Leu Leu Ile Gly Arg Ala Gln
 35 40 45

PH-1064PCT-US seq.TXT

Lys	Leu	Ser	Val	Thr	Ser	Thr	Cys	Gly	Leu	His	Lys	Pro	Glu	Pro	Tyr
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Cys	Ile	Val	Ser	His	Leu	Gln	Glu	Asp	Lys	Lys	Cys	Phe	Ile	Cys	Asn
65					70					75				80	
Ser	Gln	Asp	Pro	Tyr	His	Glu	Thr	Leu	Asn	Pro	Asp	Ser	His	Leu	Ile
				85					90					95	
Glu	Asn	Val	Val	Thr	Thr	Phe	Ala	Pro	Asn	Arg	Leu	Lys	Ile	Trp	Trp
			100					105					110		
Gln	Ser	Glu	Asn	Gly	Val	Glu	Asn	Val	Thr	Ile	Gln	Leu	Asp	Leu	Glu
			115					120					125		
Ala	Glu	Phe	His	Phe	Thr	His	Leu	Ile	Met	Thr	Phe	Lys	Thr	Phe	Arg
			130				135						140		
Pro	Ala	Ala	Met	Leu	Ile	Glu	Arg	Ser	Ser	Asp	Phe	Gly	Lys	Thr	Trp
145					150					155				160	
Gly	Val	Tyr	Arg	Tyr	Phe	Ala	Tyr	Asp	Cys	Glu	Ala	Ser	Phe	Pro	Gly
			165						170					175	
Ile	Ser	Thr	Gly	Pro	Met	Lys	Lys	Val	Asp	Asp	Ile	Ile	Cys	Asp	Ser
			180					185					190		
Arg	Tyr	Ser	Asp	Ile	Glu	Pro	Ser	Thr	Glu	Gly	Glu	Val	Ile	Phe	Arg
			195					200					205		
Ala	Leu	Asp	Pro	Ala	Phe	Lys	Ile	Glu	Asp	Pro	Tyr	Ser	Pro	Arg	Ile
			210					215					220		
Gln	Asn	Leu	Leu	Lys	Ile	Thr	Asn	Leu	Arg	Ile	Lys	Phe	Val	Lys	Leu
225					230					235				240	

PH-1064PCT-US seq.TXT

His	Thr	Leu	Gly	Asp	Asn	Leu	Leu	Asp	Ser	Arg	Met	Glu	Ile	Arg	Glu
				245					250					255	
Lys	Tyr	Tyr	Tyr	Ala	Val	Tyr	Asp	Met	Val	Val	Arg	Gly	Asn	Cys	Phe
				260				265					270		
Cys	Tyr	Gly	His	Ala	Ser	Glu	Cys	Ala	Pro	Val	Asp	Gly	Phe	Asn	Glu
			275					280					285		
Glu	Val	Glu	Gly	Met	Val	His	Gly	His	Cys	Met	Cys	Arg	His	Asn	Thr
			290				295					300			
Lys	Gly	Leu	Asn	Cys	Glu	Leu	Cys	Met	Asp	Phe	Tyr	His	Asp	Leu	Pro
305					310					315				320	
Trp	Arg	Pro	Ala	Glu	Gly	Arg	Asn	Ser	Asn	Ala	Cys	Lys	Lys	Cys	Asn
				325					330					335	
Cys	Asn	Glu	His	Ser	Ile	Ser	Cys	His	Phe	Asp	Met	Ala	Val	Tyr	Leu
			340					345					350		
Ala	Thr	Gly	Asn	Val	Ser	Gly	Gly	Val	Cys	Asp	Asp	Cys	Gln	His	Asn
			355					360					365		
Thr	Met	Gly	Arg	Asn	Cys	Glu	Gln	Cys	Lys	Pro	Phe	Tyr	Tyr	Gln	His
			370				375					380			
Pro	Glu	Arg	Asp	Ile	Arg	Asp	Pro	Asn	Phe	Cys	Glu	Arg	Cys	Thr	Cys
385					390					395				400	
Asp	Pro	Ala	Gly	Ser	Gln	Asn	Glu	Gly	Ile	Cys	Asp	Ser	Tyr	Thr	Asp
				405					410					415	
Phe	Ser	Thr	Gly	Leu	Ile	Ala	Gly	Gln	Cys	Arg	Cys	Lys	Leu	Asn	Val
			420					425					430		

PH-1064PCT-US seq.TXT

Glu Gly Glu His Cys Asp Val Cys Lys Glu Gly Phe Tyr Asp Leu Ser
435 440 445

Ser Glu Asp Pro Phe Gly Cys Lys Ser Cys Ala Cys Asn Pro Leu Gly
450 455 460

Thr Ile Pro Gly Gly Asn Pro Cys Asp Ser Glu Thr Gly His Cys Tyr
465 470 475 480

Cys Lys Arg Leu Val Thr Gly Gln His Cys Asp Gln Cys Leu Pro Glu
485 490 495

His Trp Gly Leu Ser Asn Asp Leu Asp Gly Cys Arg Pro Cys Asp Cys
500 505 510

Asp Leu Gly Gly Ala Leu Asn Asn Ser Cys Phe Ala Glu Ser Gly Gln
515 520 525

Cys Ser Cys Arg Pro His Met Ile Gly Arg Gln Cys Asn Glu Val Glu
530 535 540

Pro Gly Tyr Tyr Phe Ala Thr Leu Asp His Tyr Leu Tyr Glu Ala Glu
545 550 555 560

Glu Ala Asn Leu Gly Pro Gly Val Ser Ile Val Glu Arg Gln Tyr Ile
565 570 575

Gln Asp Arg Ile Pro Ser Trp Thr Gly Ala Gly Phe Val Arg Val Pro
580 585 590

Glu Gly Ala Tyr Leu Glu Phe Phe Ile Asp Asn Ile Pro Tyr Ser Met
595 600 605

Glu Tyr Asp Ile Leu Ile Arg Tyr Glu Pro Gln Leu Pro Asp His Trp
610 615 620

PH-1064PCT-US seq.TXT

Glu Lys Ala Val Ile Thr Val Gln Arg Pro Gly Arg Ile Pro Thr Ser
 625 630 635 640
 Ser Arg Cys Gly Asn Thr Ile Pro Asp Asp Asp Asn Gln Val Val Ser
 645 650 655
 Leu Ser Pro Gly Ser Arg Tyr Val Val Leu Pro Arg Pro Val Cys Phe
 660 665 670
 Glu Lys Gly Thr Asn Tyr Thr Val Arg Leu Glu Leu Pro Gln Tyr Thr
 675 680 685
 Ser Ser Asp Ser Asp Val Glu Ser Pro Tyr Thr Leu Ile Asp Ser Leu
 690 695 700
 Val Leu Met Pro Tyr Cys Lys Ser Leu Asp Ile Phe Thr Val Gly Gly
 705 710 715 720
 Ser Gly Asp Gly Val Val Thr Asn Ser Ala Trp Glu Thr Phe Gln Arg
 725 730 735
 Tyr Arg Cys Leu Glu Asn Ser Arg Ser Val Val Lys Thr Pro Met Thr
 740 745 750
 Asp Val Cys Arg Asn Ile Ile Phe Ser Ile Ser Ala Leu Leu His Gln
 755 760 765
 Thr Gly Leu Ala Cys Glu Cys Asp Pro Gln Gly Ser Leu Ser Ser Val
 770 775 780
 Cys Asp Pro Asn Gly Gly Gln Cys Gln Cys Arg Pro Asn Val Val Gly
 785 790 795 800
 Arg Thr Cys Asn Arg Cys Ala Pro Gly Thr Phe Gly Phe Gly Pro Ser
 805 810 815

PH-1064PCT-US seq.TXT

Gly	Cys	Lys	Pro	Cys	Glu	Cys	His	Leu	Gln	Gly	Ser	Val	Asn	Ala	Phe	
			820						825						830	
Cys	Asn	Pro	Val	Thr	Gly	Gln	Cys	His	Cys	Phe	Gln	Gly	Val	Tyr	Ala	
			835						840						845	
Arg	Gln	Cys	Asp	Arg	Cys	Leu	Pro	Gly	His	Trp	Gly	Phe	Pro	Ser	Cys	
			850						855						860	
Gln	Pro	Cys	Gln	Cys	Asn	Gly	His	Ala	Asp	Asp	Cys	Asp	Pro	Val	Thr	
865						870						875			880	
Gly	Glu	Cys	Leu	Asn	Cys	Gln	Asp	Tyr	Thr	Met	Gly	His	Asn	Cys	Glu	
			885						890						895	
Arg	Cys	Leu	Ala	Gly	Tyr	Tyr	Gly	Asp	Pro	Ile	Ile	Gly	Ser	Gly	Asp	
			900						905						910	
His	Cys	Arg	Pro	Cys	Pro	Cys	Pro	Asp	Gly	Pro	Asp	Ser	Gly	Arg	Gln	
			915						920						925	
Phe	Ala	Arg	Ser	Cys	Tyr	Gln	Asp	Pro	Val	Thr	Leu	Gln	Leu	Ala	Cys	
			930						935						940	
Val	Cys	Asp	Pro	Gly	Tyr	Ile	Gly	Ser	Arg	Cys	Asp	Asp	Cys	Ala	Ser	
945						950						955			960	
Gly	Tyr	Phe	Gly	Asn	Pro	Ser	Glu	Val	Gly	Gly	Ser	Cys	Gln	Pro	Cys	
			965						970						975	
Gln	Cys	His	Asn	Asn	Ile	Asp	Thr	Thr	Asp	Pro	Glu	Ala	Cys	Asp	Lys	
			980						985						990	
Glu	Thr	Gly	Arg	Cys	Leu	Lys	Cys	Leu	Tyr	His	Thr	Glu	Gly	Glu	His	
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PH-1064PCT-US seq.TXT

Cys Gln Phe Cys Arg Phe Gly Tyr Tyr Gly Asp Ala Leu Arg Gln Asp			
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Cys Arg Lys Cys Val Cys Asn Tyr Leu Gly Thr Val Gln Glu His Cys			
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Asn Gly Ser Asp Cys Gln Cys Asp Lys Ala Thr Gly Gln Cys Leu Cys			
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Leu Pro Asn Val Ile Gly Gln Asn Cys Asp Arg Cys Ala Pro Asn Thr			
1060	1065	1070	
Trp Gln Leu Ala Ser Gly Thr Gly Cys Asp Pro Cys Asn Cys Asn Ala			
1075	1080	1085	
Ala His Ser Phe Gly Pro Ser Cys Asn Glu Phe Thr Gly Gln Cys Gln			
1090	1095	1100	
Cys Met Pro Gly Phe Gly Gly Arg Thr Cys Ser Glu Cys Gln Glu Leu			
1105	1110	1115	1120
Phe Trp Gly Asp Pro Asp Val Glu Cys Arg Ala Cys Asp Cys Asp Pro			
1125	1130	1135	
Arg Gly Ile Glu Thr Pro Gln Cys Asp Gln Ser Thr Gly Gln Cys Val			
1140	1145	1150	
Cys Val Glu Gly Val Glu Gly Pro Arg Cys Asp Lys Cys Thr Arg Gly			
1155	1160	1165	
Tyr Ser Gly Val Phe Pro Asp Cys Thr Pro Cys His Gln Cys Phe Ala			
1170	1175	1180	
Leu Trp Asp Val Ile Ile Ala Glu Leu Thr Asn Arg Thr His Arg Phe			
1185	1190	1195	1200

PH-1064PCT-US seq.TXT

Leu Glu Lys Ala Lys Ala Leu Lys Ile Ser Gly Val Ile Gly Pro Tyr			
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Arg Glu Thr Val Asp Ser Val Glu Arg Lys Val Ser Glu Ile Lys Asp			
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Ile Leu Ala Gln Ser Pro Ala Ala Glu Pro Leu Lys Asn Ile Gly Asn			
1235	1240	1245	
Leu Phe Glu Glu Ala Glu Lys Leu Ile Lys Asp Val Thr Glu Met Met			
1250	1255	1260	
Ala Gln Val Glu Val Lys Leu Ser Asp Thr Thr Ser Gln Ser Asn Ser			
1265	1270	1275	1280
Thr Ala Lys Glu Leu Asp Ser Leu Gln Thr Glu Ala Glu Ser Leu Asp			
1285	1290	1295	
Asn Thr Val Lys Glu Leu Ala Glu Gln Leu Glu Phe Ile Lys Asn Ser			
1300	1305	1310	
Asp Ile Arg Gly Ala Leu Asp Ser Ile Thr Lys Tyr Phe Gln Met Ser			
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Leu Glu Ala Glu Glu Arg Val Asn Ala Ser Thr Thr Glu Pro Asn Ser			
1330	1335	1340	
Thr Val Glu Gln Ser Ala Leu Met Arg Asp Arg Val Glu Asp Val Met			
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Met Glu Arg Glu Ser Gln Phe Lys Glu Lys Gln Glu Glu Gln Ala Arg			
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Leu Leu Asp Glu Leu Ala Gly Lys Leu Gln Ser Leu Asp Leu Ser Ala			
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PH-1064PCT-US seq.TXT

Ala Ala Glu Met Thr Cys Gly Thr Pro Pro Gly Ala Ser Cys Ser Glu			
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Thr Glu Cys Gly Gly Pro Asn Cys Arg Thr Asp Glu Gly Glu Arg Lys			
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Cys Gly Gly Pro Gly Cys Gly Gly Leu Val Thr Val Ala His Asn Ala			
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Trp Gln Lys Ala Met Asp Leu Asp Gln Asp Val Leu Ser Ala Leu Ala			
1445	1450	1455	
Glu Val Glu Gln Leu Ser Lys Met Val Ser Glu Ala Lys Leu Arg Ala			
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Asp Glu Ala Lys Gln Ser Ala Glu Asp Ile Leu Leu Lys Thr Asn Ala			
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Thr Lys Glu Lys Met Asp Lys Ser Asn Glu Glu Leu Arg Asn Leu Ile			
1490	1495	1500	
Lys Gln Ile Arg Asn Phe Leu Thr Gln Asp Ser Ala Asp Leu Asp Ser			
1505	1510	1515	1520
Ile Glu Ala Val Ala Asn Glu Val Leu Lys Met Glu Met Pro Ser Thr			
1525	1530	1535	
Pro Gln Gln Leu Gln Asn Leu Thr Glu Asp Ile Arg Glu Arg Val Glu			
1540	1545	1550	
Ser Leu Ser Gln Val Glu Val Ile Leu Gln His Ser Ala Ala Asp Ile			
1555	1560	1565	
Ala Arg Ala Glu Met Leu Leu Glu Glu Ala Lys Arg Ala Ser Lys Ser			
1570	1575	1580	

PH-1064PCT-US seq.TXT

Ala Thr Asp Val Lys Val Thr Ala Asp Met Val Lys Glu Ala Leu Glu			
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Glu Ala Glu Lys Ala Gln Val Ala Ala Glu Lys Ala Ile Lys Gln Ala			
1605	1610	1615	
Asp Glu Asp Ile Gln Gly Thr Gln Asn Leu Leu Thr Ser Ile Glu Ser			
1620	1625	1630	
Glu Thr Ala Ala Ser Glu Glu Thr Leu Phe Asn Ala Ser Gln Arg Ile			
1635	1640	1645	
Ser Glu Leu Glu Arg Asn Val Glu Glu Leu Lys Arg Lys Ala Ala Gln			
1650	1655	1660	
Asn Ser Gly Glu Ala Glu Tyr Ile Glu Lys Val Val Tyr Thr Val Lys			
1665	1670	1675	1680
Gln Ser Ala Glu Asp Val Lys Lys Thr Leu Asp Gly Glu Leu Asp Glu			
1685	1690	1695	
Lys Tyr Lys Lys Val Glu Asn Leu Ile Ala Lys Lys Thr Glu Glu Ser			
1700	1705	1710	
Ala Asp Ala Arg Arg Lys Ala Glu Met Leu Gln Asn Glu Ala Lys Thr			
1715	1720	1725	
Leu Leu Ala Gln Ala Asn Ser Lys Leu Gln Leu Leu Lys Asp Leu Glu			
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Arg Lys Tyr Glu Asp Asn Gln Arg Tyr Leu Glu Asp Lys Ala Gln Glu			
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Leu Ala Arg Leu Glu Gly Glu Val Arg Ser Leu Leu Lys Asp Ile Ser			
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Gln Lys Val Ala Val Tyr Ser Thr Cys Leu

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1785

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<212> DNA

<213> Homo sapiens

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<400> 77

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Leu Ala Ala Leu Ala Val Val Thr Leu Cys Tyr Glu Ser His Glu Ser

10

15

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25

atg gaa tct tat gaa ctt aat ccc ttc att aac agg aga aat gca aat 149

Met Glu Ser Tyr Glu Leu Asn Pro Phe Ile Asn Arg Arg Asn Ala Asn

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35

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acc ttc ata tcc cct cag cag aga tgg aga gct aaa gtc caa gag agg 197

Thr Phe Ile Ser Pro Gln Gln Arg Trp Arg Ala Lys Val Gln Glu Arg

45

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Ile Arg Glu Arg Ser Lys Pro Val His Glu Leu Asn Arg Glu Ala Cys

60

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70

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Ala Ala Tyr Asn Arg Tyr Phe Arg Lys Arg Arg Gly Thr Lys

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<210> 78

<211> 103

<212> PRT

<213> Homo sapiens

<400> 78

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25

30

Pro Phe Ile Asn Arg Arg Asn Ala Asn Thr Phe Ile Ser Pro Gln Gln

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40

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PH-1064PCT-US seq.TXT

Arg Trp Arg Ala Lys Val Gln Glu Arg Ile Arg Glu Arg Ser Lys Pro

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Val His Glu Leu Asn Arg Glu Ala Cys Asp Asp Tyr Arg Leu Cys Glu

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Arg Lys Arg Arg Gly Thr Lys

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<210> 79

<211> 1775

<212> DNA

<213> Homo sapiens

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<222> (6)..(1148)

<400> 79

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15

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Leu Ala Glu Asn Ser Asp Asp Tyr Asp Leu Met Tyr Val Asn Leu Asp

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PH-1064PCT-US seq.TXT

Asn Glu Ile Asp Asn Gly Leu His Pro Thr Glu Asp Pro Thr Pro Cys

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Ala Cys Gly Gln Glu His Ser Glu Trp Asp Lys Leu Phe Ile Met Leu

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Glu Asn Ser Gln Met Arg Glu Arg Met Leu Leu Gln Ala Thr Asp Asp

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gtc ctg cgg ggc gag ctg cag agg ctg cgg gag gag ctg ggc cgg ctc 290

Val Leu Arg Gly Glu Leu Gln Arg Leu Arg Glu Glu Leu Gly Arg Leu

80

85

90

95

gcg gaa agc ctg gcg agg ccg tgc gcg ccg ggg gct ccc gca gag gcc 338

Ala Glu Ser Leu Ala Arg Pro Cys Ala Pro Gly Ala Pro Ala Glu Ala

100

105

110

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115

120

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Gly Arg Arg Leu Ala Arg Met Glu Gly Ala Glu Ala Gln Arg Pro Glu

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135

140

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Ser	Ala	Cys	Ile	Trp	Val	Lys	Ala	Thr	Asp	Val	Leu	Asn	Lys	Thr	Ile		
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Leu	Phe	Ser	Tyr	Gly	Thr	Lys	Arg	Asn	Pro	Tyr	Glu	Ile	Gln	Leu	Tyr		
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ctc	agc	tac	caa	tcc	ata	gtg	ttt	gtg	gtg	ggt	gga	gag	gag	aac	aaa	770	
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ctg	gtt	gct	gaa	gcc	atg	gtt	tcc	ctg	gga	agg	tgg	acc	cac	ctg	tgc	818	
Leu	Val	Ala	Glu	Ala	Met	Val	Ser	Leu	Gly	Arg	Trp	Thr	His	Leu	Cys		
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ggc	acc	tgg	aat	tca	gag	gaa	ggg	ctc	aca	tcc	ttg	tgg	gta	aat	ggt	866	
Gly	Thr	Trp	Asn	Ser	Glu	Glu	Gly	Leu	Thr	Ser	Leu	Trp	Val	Asn	Gly		
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Glu Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro

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<211> 381

<212> PRT

<213> Homo sapiens

<400> 80

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145	150	155
Ala Asp Leu His Ala Val Gln Gly Trp Ala Ala Arg Ser Trp Leu Pro		
165	170	175
Ala Gly Cys Glu Thr Ala Ile Leu Phe Pro Met Arg Ser Lys Lys Ile		
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Phe Gly Ser Val His Pro Val Arg Pro Met Arg Leu Glu Ser Phe Ser		
195	200	205
Ala Cys Ile Trp Val Lys Ala Thr Asp Val Leu Asn Lys Thr Ile Leu		
210	215	220
Phe Ser Tyr Gly Thr Lys Arg Asn Pro Tyr Glu Ile Gln Leu Tyr Leu		
225	230	235
Ser Tyr Gln Ser Ile Val Phe Val Val Gly Gly Glu Glu Asn Lys Leu		
245	250	255
Val Ala Glu Ala Met Val Ser Leu Gly Arg Trp Thr His Leu Cys Gly		
260	265	270
Thr Trp Asn Ser Glu Glu Gly Leu Thr Ser Leu Trp Val Asn Gly Glu		
275	280	285
Leu Ala Ala Thr Thr Val Glu Met Ala Thr Gly His Ile Val Pro Glu		
290	295	300
Gly Gly Ile Leu Gln Ile Gly Gln Glu Lys Asn Gly Cys Cys Val Gly		

PH-1064PCT-US seq.TXT

305	310	315	320
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Asn Ile Trp Asp Ser Val Leu Ser Asn Glu Glu Ile Arg Glu Thr Gly			
	340	345	350
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<211> 2312

<212> DNA

<213> Homo sapiens

<220>

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<222> (146)..(1192)

<400> 81

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Met Thr Ala Ala Ser Met Gly Pro Val

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cgc	tgc	ccg	gcg	ggc	gtg	agc	ctc	gtg	ctg	gac	ggc	tgc	ggc	tgc	tgc	316
Arg	Cys	Pro	Ala	Gly	Val	Ser	Leu	Val	Leu	Asp	Gly	Cys	Gly	Cys	Cys	
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Cys	Asp	Pro	His	Lys	Gly	Leu	Phe	Cys	Asp	Phe	Gly	Ser	Pro	Ala	Asn	
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Arg	Lys	Ile	Gly	Val	Cys	Thr	Ala	Lys	Asp	Gly	Ala	Pro	Cys	Ile	Phe	
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tac	cag	tgc	acg	tgc	ctg	gac	ggg	gcg	gtg	ggc	tgc	atg	ccc	ctg	tgc	556
Tyr	Gln	Cys	Thr	Cys	Leu	Asp	Gly	Ala	Val	Gly	Cys	Met	Pro	Leu	Cys	
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155	160	165	
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Lys Asp Gln Thr Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu			
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gac acg ttt ggc cca gac cca act atg att aga gcc aac tgc ctg gtc			748
Asp Thr Phe Gly Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val			
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Gln Thr Thr Glu Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile			
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Ser Thr Arg Val Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln			
	220	225	230
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Ser Arg Leu Cys Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn			
	235	240	245
att aag aag ggc aaa aag tgc atc cgt act ccc aaa atc tcc aag cct			940
Ile Lys Lys Gly Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro			
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PH-1064PCT-US seq.TXT

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285

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295

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305

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340

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<211> 349

<212> PRT

<213> Homo sapiens

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Met Asp

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Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala Asp Met
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Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile Asn Pro
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Leu Pro Pro Gln Gln Glu Trp Ile Asn Gln Pro Val Arg Val Asn Val
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Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro Val Asp
      70              75              80
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Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu Ser Asn
      85              90              95
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Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro Pro Pro
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ccc aac atg acc acc aac gag agg aga gtc atc gtc ccc gca gac ccc 562
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Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln Asn Met
          150          155          160
gat ggc aag gaa ctg tgt aaa atg aac aag gag gac ttc ctc cgc gcc 706
Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu Arg Ala
          165          170          175
acc acc ctc tac aac acg gaa gtg ctg ttg tca cac ctc agt tac ctc 754
Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser Tyr Leu
          180          185          190
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Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr Asp Gln
195          200          205          210
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aac cct gga agc ggg cag atc cag ctg tgg caa ttc ctc ctg gag ctg			1042
Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu			
275	280	285	290
ctc tcc gac agc gcc aac gcc agc tgt atc acc tgg gag ggg acc aac			1090
Leu Ser Asp Ser Ala Asn Ala Ser Cys Ile Thr Trp Glu Gly Thr Asn			
	295	300	305
ggg gag ttc aaa atg acg gac ccc gat gag gtg gcc agg cgc tgg ggc			1138
Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly			
	310	315	320
gag cgg aaa agc aag ccc aac atg aat tac gac aag ctg agc cgg gcc			1186
Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala			
	325	330	335
ctc cgt tat tac tat gat aaa aac att atg acc aaa gtg cac ggc aaa			1234
Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Gly Lys			
	340	345	350
aga tat gct tac aaa ttt gac ttc cac ggc att gcc cag gct ctg cag			1282
Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln Ala Leu Gln			
355	360	365	370
cca cat ccg acc gag tcg tcc atg tac aag tac cct tct gac atc tcc			1330
Pro His Pro Thr Glu Ser Ser Met Tyr Lys Tyr Pro Ser Asp Ile Ser			

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tac atg cct tcc caa cat gcc cac cag cag aag gtg aac ttt gtc cct 1378
Tyr Met Pro Ser Gln His Ala His Gln Gln Lys Val Asn Phe Val Pro

390                               395                               400
ccc cat cca tcc tcc atg cct gtc act tcc tcc agc ttc ttt gga gcc 1426
Pro His Pro Ser Ser Met Pro Val Thr Ser Ser Ser Phe Phe Gly Ala

405                               410                               415
gca tca caa tac tgg acc tcc acg ggg gga atc tac ccc aac ccc aac 1474
Ala Ser Gln Tyr Trp Thr Ser Thr Gly Gly Ile Tyr Pro Asn Pro Asn

420                               425                               430
gtc ccc cgc cat cct aac acc cac gtg cct tca cac tta ggc agc tac 1522
Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly Ser Tyr

435                               440                               445                               450
tac tagaagctta ctcatcagtg gccttctagc tgaagcccat cctgcacact 1575
Tyr

tactggatgc tttggactca acaggacata tgtggccttg aagggaagac aaaactggat 1635
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<210> 84

<211> 451

<212> PRT

<213> Homo sapiens

<400> 84

Met Asp Gly Thr Ile Lys Glu Ala Leu Ser Val Val Ser Asp Asp Gln

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10

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Ser Leu Phe Asp Ser Ala Tyr Gly Ala Ala Ala His Leu Pro Lys Ala

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25

30

Asp Met Thr Ala Ser Gly Ser Pro Asp Tyr Gly Gln Pro His Lys Ile

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35	40	45
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Asn Val Lys Arg Glu Tyr Asp His Met Asn Gly Ser Arg Glu Ser Pro		
65	70	75
Val Asp Cys Ser Val Ser Lys Cys Ser Lys Leu Val Gly Gly Gly Glu		
85	90	95
Ser Asn Pro Met Asn Tyr Asn Ser Tyr Met Asp Glu Lys Asn Gly Pro		
100	105	110
Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro Ala		
115	120	125
Asp Pro Thr Leu Trp Thr Gln Glu His Val Arg Gln Trp Leu Glu Trp		
130	135	140
Ala Ile Lys Glu Tyr Ser Leu Met Glu Ile Asp Thr Ser Phe Phe Gln		
145	150	155
Asn Met Asp Gly Lys Glu Leu Cys Lys Met Asn Lys Glu Asp Phe Leu		
165	170	175
Arg Ala Thr Thr Leu Tyr Asn Thr Glu Val Leu Leu Ser His Leu Ser		
180	185	190
Tyr Leu Arg Glu Ser Ser Leu Leu Ala Tyr Asn Thr Thr Ser His Thr		
195	200	205
Asp Gln Ser Ser Arg Leu Ser Val Lys Glu Asp Pro Ser Tyr Asp Ser		
210	215	220
Val Arg Arg Gly Ala Trp Gly Asn Asn Met Asn Ser Gly Leu Asn Lys		

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Arg	Pro	Gln	Pro	Asp	Pro	Tyr	Gln	Ile	Leu	Gly	Pro	Thr	Ser	Ser	Arg
		260		265		270									
Leu	Ala	Asn	Pro	Gly	Ser	Gly	Gln	Ile	Gln	Leu	Trp	Gln	Phe	Leu	Leu
		275		280		285									
Glu	Leu	Leu	Ser	Asp	Ser	Ala	Asn	Ala	Ser	Cys	Ile	Thr	Trp	Glu	Gly
		290		295		300									
Thr	Asn	Gly	Glu	Phe	Lys	Met	Thr	Asp	Pro	Asp	Glu	Val	Ala	Arg	Arg
305		310		315		320									
Trp	Gly	Glu	Arg	Lys	Ser	Lys	Pro	Asn	Met	Asn	Tyr	Asp	Lys	Leu	Ser
		325		330		335									
Arg	Ala	Leu	Arg	Tyr	Tyr	Tyr	Asp	Lys	Asn	Ile	Met	Thr	Lys	Val	His
		340		345		350									
Gly	Lys	Arg	Tyr	Ala	Tyr	Lys	Phe	Asp	Phe	His	Gly	Ile	Ala	Gln	Ala
		355		360		365									
Leu	Gln	Pro	His	Pro	Thr	Glu	Ser	Ser	Met	Tyr	Lys	Tyr	Pro	Ser	Asp
		370		375		380									
Ile	Ser	Tyr	Met	Pro	Ser	Gln	His	Ala	His	Gln	Gln	Lys	Val	Asn	Phe
385		390		395		400									
Val	Pro	Pro	His	Pro	Ser	Ser	Met	Pro	Val	Thr	Ser	Ser	Ser	Phe	Phe
		405		410		415									
Gly	Ala	Ala	Ser	Gln	Tyr	Trp	Thr	Ser	Thr	Gly	Gly	Ile	Tyr	Pro	Asn

PH-1064PCT-US seq.TXT

420

425

430

Pro Asn Val Pro Arg His Pro Asn Thr His Val Pro Ser His Leu Gly

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440

445

Ser Tyr Tyr

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<210> 85

<211> 1817

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(361)

<400> 85

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15

agg cct gca ggg gat gga acc ttc cag aag tgg gca gct gtg gtg gtg 97

Arg Pro Ala Gly Asp Gly Thr Phe Gln Lys Trp Ala Ala Val Val Val

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25

30

cct tct gga gag gag cag aga tac acg tgc cat gtg cag cat gag ggg 145

Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

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cta ccc gag ccc gtc acc ctg aga tgg aag ccg gct tcc cag ccc acc 193

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Leu Pro Glu Pro Val Thr Leu Arg Trp Lys Pro Ala Ser Gln Pro Thr
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atc ccc atc gtg ggc atc att gct ggc ctg gtt ctc ctt gga tct gtg 241
Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val
65 70 75 80
gtc tct gga gct gtg gtt gct gct gtg ata tgg agg aag aag agc tca 289
Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser
85 90 95
ggg gga aaa gga ggg agc tac tct aag gct gag tgg agc gac agt gcc 337
Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala
100 105 110
cag ggg tct gag tct cac agc ttg taaagcctga gacagctgcc ttgtgtgcga 391
Gln Gly Ser Glu Ser His Ser Leu
115 120
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<210> 86

<211> 120

<212> PRT

<213> Homo sapiens

<400> 86

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Pro Ser Gly Glu Glu Gln Arg Tyr Thr Cys His Val Gln His Glu Gly

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Ile Pro Ile Val Gly Ile Ile Ala Gly Leu Val Leu Leu Gly Ser Val		
65	70	75
Val Ser Gly Ala Val Val Ala Ala Val Ile Trp Arg Lys Lys Ser Ser		
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Gly Gly Lys Gly Gly Ser Tyr Ser Lys Ala Glu Trp Ser Asp Ser Ala		
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Gln Gly Ser Glu Ser His Ser Leu		
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<211> 2876

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (76)..(1281)

<400> 87

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Met Gln Met Ser Pro Ala Leu Thr Cys Leu Val Leu

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15 20 25	
tcc tac gtg gcc cac ctg gcc tca gac ttc ggg gtg agg gtg ttt cag	207
Ser Tyr Val Ala His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln	
30 35 40	
cag gtg gcg cag gcc tcc aag gac cgc aac gtg gtt ttc tca ccc tat	255
Gln Val Ala Gln Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr	
45 50 55 60	
ggg gtg gcc tcg gtg ttg gcc atg ctc cag ctg aca aca gga gga gaa	303
Gly Val Ala Ser Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu	
65 70 75	
acc cag cag cag att caa gca gct atg gga ttc aag att gat gac aag	351
Thr Gln Gln Gln Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys	
80 85 90	
ggc atg gcc ccc gcc ctc cgg cat ctg tac aag gag ctc atg ggg cca	399
Gly Met Ala Pro Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro	
95 100 105	
tgg aac aag gat gag atc agc acc aca gac gcg atc ttc gtc cag cgg	447
Trp Asn Lys Asp Glu Ile Ser Thr Thr Asp Ala Ile Phe Val Gln Arg	
110 115 120	
gat ctg aag ctg gtc cag ggc ttc atg ccc cac ttc ttc agg ctg ttc	495
Asp Leu Lys Leu Val Gln Gly Phe Met Pro His Phe Phe Arg Leu Phe	
125 130 135 140	

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Phe Ile Ile Asn Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser	
160 165 170	
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Asn Leu Leu Gly Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu	
175 180 185	
gtg aat gcc ctc tac ttc aac ggc cag tgg aag act ccc ttc ccc gac	687
Val Asn Ala Leu Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp	
190 195 200	
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Ser Ser Thr His Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val	
205 210 215 220	
tct gtg ccc atg atg gct cag acc aac aag ttc aac tat act gag ttc	783
Ser Val Pro Met Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe	
225 230 235	
acc acg ccc gat ggc cat tac tac gac atc ctg gaa ctg ccc tac cac	831
Thr Thr Pro Asp Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His	
240 245 250	
ggg gac acc ctc agc atg ttc att gct gcc cct tat gaa aaa gag gtg	879
Gly Asp Thr Leu Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val	
255 260 265	

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tgg aaa ggc aac atg acc agg ctg ccc cgc ctc ctg gtt ctg ccc aag	975
Trp Lys Gly Asn Met Thr Arg Leu Pro Arg Leu Leu Val Leu Pro Lys	
285 290 295 300	
ttc tcc ctg gag act gaa gtc gac ctc agg aag ccc cta gag aac ctg	1023
Phe Ser Leu Glu Thr Glu Val Asp Leu Arg Lys Pro Leu Glu Asn Leu	
305 310 315	
gga atg acc gac atg ttc aga cag ttt cag gct gac ttc acg agt ctt	1071
Gly Met Thr Asp Met Phe Arg Gln Phe Gln Ala Asp Phe Thr Ser Leu	
320 325 330	
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Ser Asp Gln Glu Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys	
335 340 345	
atc gag gtg aac gag agt ggc acg gtg gcc tcc tca tcc aca gct gtc	1167
Ile Glu Val Asn Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val	
350 355 360	
ata gtc tca gcc cgc atg gcc ccc gag gag atc atc atg gac aga ccc	1215
Ile Val Ser Ala Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro	
365 370 375 380	
ttc ctc ttt gtg gtc cgg cac aac ccc aca gga aca gtc ctt ttc atg	1263
Phe Leu Phe Val Val Arg His Asn Pro Thr Gly Thr Val Leu Phe Met	
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Gly Gln Val Met Glu Pro

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gactctttct gaaggaagag aagacatttg ccttttggtta aaagatggta aaccagatct 1431

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<210> 88

<211> 402

<212> PRT

<213> Homo sapiens

<400> 88

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His Leu Ala Ser Asp Phe Gly Val Arg Val Phe Gln Gln Val Ala Gln
35 40 45
Ala Ser Lys Asp Arg Asn Val Val Phe Ser Pro Tyr Gly Val Ala Ser
50 55 60
Val Leu Ala Met Leu Gln Leu Thr Thr Gly Gly Glu Thr Gln Gln Gln
65 70 75 80
Ile Gln Ala Ala Met Gly Phe Lys Ile Asp Asp Lys Gly Met Ala Pro
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Ala Leu Arg His Leu Tyr Lys Glu Leu Met Gly Pro Trp Asn Lys Asp

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130		135		140
Lys Gln Val Asp Phe Ser Glu Val Glu Arg Ala Arg Phe Ile Ile Asn				
145		150		155
Asp Trp Val Lys Thr His Thr Lys Gly Met Ile Ser Asn Leu Leu Gly				
	165		170	
Lys Gly Ala Val Asp Gln Leu Thr Arg Leu Val Leu Val Asn Ala Leu				
	180		185	
Tyr Phe Asn Gly Gln Trp Lys Thr Pro Phe Pro Asp Ser Ser Thr His				
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Arg Arg Leu Phe His Lys Ser Asp Gly Ser Thr Val Ser Val Pro Met				
	210		215	
Met Ala Gln Thr Asn Lys Phe Asn Tyr Thr Glu Phe Thr Thr Pro Asp				
225		230		235
Gly His Tyr Tyr Asp Ile Leu Glu Leu Pro Tyr His Gly Asp Thr Leu				
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Ser Met Phe Ile Ala Ala Pro Tyr Glu Lys Glu Val Pro Leu Ser Ala				
	260		265	
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290
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Pro Leu His Val Ala Gln Ala Leu Gln Lys Val Lys Ile Glu Val Asn
340 345 350
Glu Ser Gly Thr Val Ala Ser Ser Ser Thr Ala Val Ile Val Ser Ala
355 360 365
Arg Met Ala Pro Glu Glu Ile Ile Met Asp Arg Pro Phe Leu Phe Val
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<210> 89

<211> 1412

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (52)..(1341)

<400> 89

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PH-1064PCT-US seq.TXT

Met Ser

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Phe Thr Thr Arg Ser Thr Phe Ser Thr Asn Tyr Arg Ser Leu Gly Ser

5

10

15

gtc cag gcg ccc agc tac ggc gcc cgg ccg gtc agc agc gcg gcc agc 153

Val Gln Ala Pro Ser Tyr Gly Ala Arg Pro Val Ser Ser Ala Ala Ser

20

25

30

gtc tat gca ggc gct ggg ggc tct ggt tcc cgg atc tcc gtg tcc cgc 201

Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val Ser Arg

35

40

45

50

tcc acc agc ttc agg ggc ggc atg ggg tcc ggg ggc ctg gcc acc ggg 249

Ser Thr Ser Phe Arg Gly Gly Met Gly Ser Gly Gly Leu Ala Thr Gly

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ata gcc ggg ggt ctg gca gga atg gga ggc atc cag aac gag aag gag 297

Ile Ala Gly Gly Leu Ala Gly Met Gly Gly Ile Gln Asn Glu Lys Glu

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75

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acc atg caa agc ctg aac gac cgc ctg gcc tct tac ctg gac aga gtg 345

Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp Arg Val

85

90

95

agg agc ctg gag acc gag aac cgg agg ctg gag agc aaa atc cgg gag 393

Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile Arg Glu

100

105

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cac ttg gag aag aag gga ccc cag gtc aga gac tgg agc cat tac ttc 441

PH-1064PCT-US seq.TXT

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Lys	Ile	Ile	Glu	Asp	Leu	Arg	Ala	Gln	Ile	Phe	Ala	Asn	Thr	Val	Asp		
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aat	gcc	cgc	atc	gtt	ctg	cag	att	gac	aat	gcc	cgt	ctt	gct	gct	gat	537	
Asn	Ala	Arg	Ile	Val	Leu	Gln	Ile	Asp	Asn	Ala	Arg	Leu	Ala	Ala	Asp		
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gac	ttt	aga	gtc	aag	tat	gag	aca	gag	ctg	gcc	atg	cgc	cag	tct	gtg	585	
Asp	Phe	Arg	Val	Lys	Tyr	Glu	Thr	Glu	Leu	Ala	Met	Arg	Gln	Ser	Val		
			165					170						175			
gag	aac	gac	atc	cat	ggg	ctc	cgc	aag	gtc	att	gat	gac	acc	aat	atc	633	
Glu	Asn	Asp	Ile	His	Gly	Leu	Arg	Lys	Val	Ile	Asp	Asp	Thr	Asn	Ile		
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aca	cga	ctg	cag	ctg	gag	aca	gag	atc	gag	gct	ctc	aag	gag	gag	ctg	681	
Thr	Arg	Leu	Gln	Leu	Glu	Thr	Glu	Ile	Glu	Ala	Leu	Lys	Glu	Glu	Leu		
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ctc	ttc	atg	aag	aag	aac	cac	gaa	gag	gaa	gta	aaa	ggc	cta	caa	gcc	729	
Leu	Phe	Met	Lys	Lys	Asn	His	Glu	Glu	Glu	Val	Lys	Gly	Leu	Gln	Ala		
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cag	att	gcc	agc	tct	ggg	ttg	acc	gtg	gag	gta	gat	gcc	ccc	aaa	tct	777	
Gln	Ile	Ala	Ser	Ser	Gly	Leu	Thr	Val	Glu	Val	Asp	Ala	Pro	Lys	Ser		
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PH-1064PCT-US seq.TXT

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att gag gag agc acc aca gtg gtc acc aca cag tct gct gag gtt gga	921		
Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu Val Gly			
275	280	285	290
gct gct gag acg acg ctc aca gag ctg aga cgt aca gtc cag tcc ttg	969		
Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln Ser Leu			
295	300	305	
gag atc gac ctg gac tcc atg aga aat ctg aag gcc agc ttg gag aac	1017		
Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu Glu Asn			
310	315	320	
agc ctg agg gag gtg gag gcc cgc tac gcc cta cag atg gag cag ctc	1065		
Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu Gln Leu			
325	330	335	
aac ggg atc ctg ctg cac ctt gag tca gag ctg gca cag acc cgg gca	1113		
Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr Arg Ala			
340	345	350	
gag gga cag cgc cag gcc cag gag tat gag gcc ctg ctg aac atc aag	1161		
Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn Ile Lys			
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gtc aag ctg gag gct gag atc gcc acc tac cgc cgc ctg ctg gaa gat	1209		

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Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu Glu Asp
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Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn Ser Met
390 395 400
caa acc atc caa aag acc acc acc cgc cgg ata gtg gat ggc aaa gtg 1305
Gln Thr Ile Gln Lys Thr Thr Thr Arg Arg Ile Val Asp Gly Lys Val
405 410 415
gtg tct gag acc aat gac acc aaa gtt ctg agg cat taagccagca 1351
Val Ser Glu Thr Asn Asp Thr Lys Val Leu Arg His
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<210> 90

<211> 430

<212> PRT

<213> Homo sapiens

<400> 90

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Ala Ser Val Tyr Ala Gly Ala Gly Gly Ser Gly Ser Arg Ile Ser Val

PH-1064PCT-US seq.TXT

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				80
Lys Glu Thr Met Gln Ser Leu Asn Asp Arg Leu Ala Ser Tyr Leu Asp				
	85		90	95
Arg Val Arg Ser Leu Glu Thr Glu Asn Arg Arg Leu Glu Ser Lys Ile				
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Arg Glu His Leu Glu Lys Lys Gly Pro Gln Val Arg Asp Trp Ser His				
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Tyr Phe Lys Ile Ile Glu Asp Leu Arg Ala Gln Ile Phe Ala Asn Thr				
	130		135	140
Val Asp Asn Ala Arg Ile Val Leu Gln Ile Asp Asn Ala Arg Leu Ala				
145		150		155
				160
Ala Asp Asp Phe Arg Val Lys Tyr Glu Thr Glu Leu Ala Met Arg Gln				
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Ser Val Glu Asn Asp Ile His Gly Leu Arg Lys Val Ile Asp Asp Thr				
	180		185	190
Asn Ile Thr Arg Leu Gln Leu Glu Thr Glu Ile Glu Ala Leu Lys Glu				
	195		200	205
Glu Leu Leu Phe Met Lys Lys Asn His Glu Glu Glu Val Lys Gly Leu				
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Gln Ala Gln Ile Ala Ser Ser Gly Leu Thr Val Glu Val Asp Ala Pro				

PH-1064PCT-US seq.TXT

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225                230                235                240
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Asp Glu Leu Ala Arg Lys Asn Arg Glu Glu Leu Asp Lys Tyr Trp Ser

                260                265                270
Gln Gln Ile Glu Glu Ser Thr Thr Val Val Thr Thr Gln Ser Ala Glu

                275                280                285
Val Gly Ala Ala Glu Thr Thr Leu Thr Glu Leu Arg Arg Thr Val Gln

                290                295                300
Ser Leu Glu Ile Asp Leu Asp Ser Met Arg Asn Leu Lys Ala Ser Leu

305                310                315                320
Glu Asn Ser Leu Arg Glu Val Glu Ala Arg Tyr Ala Leu Gln Met Glu

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Gln Leu Asn Gly Ile Leu Leu His Leu Glu Ser Glu Leu Ala Gln Thr

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Arg Ala Glu Gly Gln Arg Gln Ala Gln Glu Tyr Glu Ala Leu Leu Asn

                355                360                365
Ile Lys Val Lys Leu Glu Ala Glu Ile Ala Thr Tyr Arg Arg Leu Leu

                370                375                380
Glu Asp Gly Glu Asp Phe Asn Leu Gly Asp Ala Leu Asp Ser Ser Asn

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<222> (171)..(968)

<400> 91

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tcc cag ctg gag ctg ctg agt ggg gga gag atg ctg tgc ggt ggc ttc 224
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15

tac cct cgg ctg tcc tgc tgc ctg cgg agt gac agc ccg ggg cta ggg 272
Tyr Pro Arg Leu Ser Cys Cys Leu Arg Ser Asp Ser Pro Gly Leu Gly

20

25

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cgc ctg gag aat aag ata ttt tct gtt acc aac aac aca gaa tgt ggg 320
Arg Leu Glu Asn Lys Ile Phe Ser Val Thr Asn Asn Thr Glu Cys Gly

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PH-1064PCT-US seq.TXT

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Leu	Pro	Leu	Leu	Cys	Lys	Asp	Tyr	Cys	Lys	Glu	Phe	Phe	Tyr	Thr	Cys		
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cga	ggc	cat	att	cca	ggg	ttc	ctt	caa	aca	act	gcg	gat	gag	ttt	tgc	512	
Arg	Gly	His	Ile	Pro	Gly	Phe	Leu	Gln	Thr	Thr	Ala	Asp	Glu	Phe	Cys		
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Phe	Tyr	Tyr	Ala	Arg	Lys	Asp	Gly	Gly	Leu	Cys	Phe	Pro	Asp	Phe	Pro		
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Arg	Lys	Gln	Val	Arg	Gly	Pro	Ala	Ser	Asn	Tyr	Leu	Asp	Gln	Met	Glu		
135					140					145							
gaa	tat	gac	aaa	gtg	gaa	gag	atc	agc	aga	aag	cac	aaa	cac	aac	tgc	656	
Glu	Tyr	Asp	Lys	Val	Glu	Glu	Ile	Ser	Arg	Lys	His	Lys	His	Asn	Cys		
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Phe	Cys	Ile	Gln	Glu	Val	Val	Ser	Gly	Leu	Arg	Gln	Pro	Val	Gly	Ala		
165					170					175							
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 Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys Glu Pro
 195 200 205 210
 tat ttg gac att cac aaa ctt gtt caa agt gga ata aag gtt ggc ttt 848
 Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val Gly Phe
 215 220 225
 tta aat ttt att tat ttt tgt gct ggc tac gtt aat ttt att tta gtg 896
 Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile Leu Val
 230 235 240
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 Leu Pro Ser Ser Leu Lys Val Phe Leu Cys Asn Lys Arg Lys Asn Leu
 245 250 255
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<211> 266

<212> PRT

<213> Homo sapiens

<400> 92

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Gly	Phe	Tyr	Pro	Arg	Leu	Ser	Cys	Cys	Leu	Arg	Ser	Asp	Ser	Pro	Gly
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Leu	Gly	Arg	Leu	Glu	Asn	Lys	Ile	Phe	Ser	Val	Thr	Asn	Asn	Thr	Glu
			35				40						45		
Cys	Gly	Lys	Leu	Leu	Glu	Glu	Ile	Lys	Cys	Ala	Leu	Cys	Ser	Pro	His
	50						55					60			
Ser	Gln	Ser	Leu	Phe	His	Ser	Pro	Glu	Arg	Glu	Val	Leu	Glu	Arg	Asp
65					70					75					80
Leu	Val	Leu	Pro	Leu	Leu	Cys	Lys	Asp	Tyr	Cys	Lys	Glu	Phe	Phe	Tyr
					85					90				95	
Thr	Cys	Arg	Gly	His	Ile	Pro	Gly	Phe	Leu	Gln	Thr	Thr	Ala	Asp	Glu
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Phe	Cys	Phe	Tyr	Tyr	Ala	Arg	Lys	Asp	Gly	Gly	Leu	Cys	Phe	Pro	Asp
		115						120					125		
Phe	Pro	Arg	Lys	Gln	Val	Arg	Gly	Pro	Ala	Ser	Asn	Tyr	Leu	Asp	Gln
		130					135						140		
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Asn	Cys	Phe	Cys	Ile	Gln	Glu	Val	Val	Ser	Gly	Leu	Arg	Gln	Pro	Val
				165						170				175	
Gly	Ala	Leu	His	Ser	Gly	Asp	Gly	Ser	Gln	Arg	Leu	Phe	Ile	Leu	Glu
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Lys Glu Gly Tyr Val Lys Ile Leu Thr Pro Glu Gly Glu Ile Phe Lys

195

200

205

Glu Pro Tyr Leu Asp Ile His Lys Leu Val Gln Ser Gly Ile Lys Val

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215

220

Gly Phe Leu Asn Phe Ile Tyr Phe Cys Ala Gly Tyr Val Asn Phe Ile

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<210> 93

<211> 1639

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (75)..(371)

<400> 93

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Met Thr Ser Lys Leu Ala Val Ala Leu Leu Ala Ala

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10

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cac ccc aaa ttt atc aaa gaa ctg aga gtg att gag agt gga cca cac			254
His Pro Lys Phe Ile Lys Glu Leu Arg Val Ile Glu Ser Gly Pro His			
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tgc gcc aac aca gaa att att gta aag ctt tct gat gga aga gag ctc			302
Cys Ala Asn Thr Glu Ile Ile Val Lys Leu Ser Asp Gly Arg Glu Leu			
	65	70	75
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Cys Leu Asp Pro Lys Glu Asn Trp Val Gln Arg Val Val Glu Lys Phe			
80	85	90	
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Leu Lys Arg Ala Glu Asn Ser			
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aaatgatggg acaataaatt ttgccataaa gtcaaattta gctggaaatc ctggattttt			821
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<210> 94

<211> 99

<212> PRT

<213> Homo sapiens

<400> 94

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				20					25					30	
Arg	Cys	Gln	Cys	Ile	Lys	Thr	Tyr	Ser	Lys	Pro	Phe	His	Pro	Lys	Phe

PH-1064PCT-US seq.TXT

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Glu	Ile	Ile	Val	Lys	Leu	Ser	Asp	Gly	Arg	Glu	Leu	Cys	Leu	Asp	Pro
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Lys	Glu	Asn	Trp	Val	Gln	Arg	Val	Val	Glu	Lys	Phe	Leu	Lys	Arg	Ala
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<212> DNA

<213> Homo sapiens

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<222> (8)..(1945)

<400> 95

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Cys	Cys	Cys	Cys	Pro	Arg	Val	Ala	Gly	Val	Pro	Gly	Glu	Ala	Glu	Gln	
15		20		25		30										
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Gly Gln Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu				
	80	85	90	
cag gac aga ggg gct act ctg gcc ctg act caa gtc acc ccc caa gac				337
Gln Asp Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp				
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Glu Arg Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr				
	115	120	125	
cgc atc cag ctc cgc gtc tac aaa gct ccg gag gag cca aac atc cag				433
Arg Ile Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln				
	130	135	140	
gtc aac ccc ctg ggc atc cct gtg aac agt aag gag cct gag gag gtc				481
Val Asn Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val				
	145	150	155	
gct acc tgt gta ggg agg aac ggg tac ccc att cct caa gtc atc tgg				529
Ala Thr Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp				

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175	180	185	190
cag tcg tcc cag act gtg gag tcg agt ggt ttg tac acc ttg cag agt	625		
Gln Ser Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser			
195	200	205	
att ctg aag gca cag ctg gtt aaa gaa gac aaa gat gcc cag ttt tac	673		
Ile Leu Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr			
210	215	220	
tgt gag ctc aac tac cgg ctg ccc agt ggg aac cac atg aag gag tcc	721		
Cys Glu Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser			
225	230	235	
agg gaa gtc acc gtc cct gtt ttc tac ccg aca gaa aaa gtg tgg ctg	769		
Arg Glu Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu			
240	245	250	
gaa gtg gag ccc gtg gga atg ctg aag gaa ggg gac cgc gtg gaa atc	817		
Glu Val Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile			
255	260	265	270
agg tgt ttg gct gat ggc aac cct cca cca cac ttc agc atc agc aag	865		
Arg Cys Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys			
275	280	285	
cag aac ccc agc acc agg gag gca gag gaa gag aca acc aac gac aac	913		
Gln Asn Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn			

PH-1064PCT-US seq.TXT

290	295	300	
ggg gtc ctg gtg ctg gag cct gcc cgg aag gaa cac agt ggg cgc tat			961
Gly Val Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr			
305	310	315	
gaa tgt cag gcc tgg aac ttg gac acc atg ata tcg ctg ctg agt gaa			1009
Glu Cys Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu			
320	325	330	
cca cag gaa cta ctg gtg aac tat gtg tct gac gtc cga gtg agt ccc			1057
Pro Gln Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro			
335	340	345	350
gca gcc cct gag aga cag gaa ggc agc agc ctc acc ctg acc tgt gag			1105
Ala Ala Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu			
355	360	365	
gca gag agt agc cag gac ctc gag ttc cag tgg ctg aga gaa gag aca			1153
Ala Glu Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr			
370	375	380	
gac cag gtg ctg gaa agg ggg cct gtg ctt cag ttg cat gac ctg aaa			1201
Asp Gln Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys			
385	390	395	
cgg gag gca gga ggc ggc tat cgc tgc gtg gcg tct gtg ccc agc ata			1249
Arg Glu Ala Gly Gly Gly Tyr Arg Cys Val Ala Ser Val Pro Ser Ile			
400	405	410	
ccc ggc ctg aac cgc aca cag ctg gtc aag ctg gcc att ttt ggc ccc			1297
Pro Gly Leu Asn Arg Thr Gln Leu Val Lys Leu Ala Ile Phe Gly Pro			

PH-1064PCT-US seq.TXT

415	420	425	430	
cct tgg atg gca ttc aag gag agg aag gtg tgg gtg aaa gag aat atg				1345
Pro Trp Met Ala Phe Lys Glu Arg Lys Val Trp Val Lys Glu Asn Met				
	435	440	445	
gtg ttg aat ctg tct tgt gaa gcg tca ggg cac ccc cgg ccc acc atc				1393
Val Leu Asn Leu Ser Cys Glu Ala Ser Gly His Pro Arg Pro Thr Ile				
	450	455	460	
tcc tgg aac gtc aac ggc acg gca agt gaa caa gac caa gat cca cag				1441
Ser Trp Asn Val Asn Gly Thr Ala Ser Glu Gln Asp Gln Asp Pro Gln				
	465	470	475	
cga gtc ctg agc acc ctg aat gtc ctc gtg acc ccg gag ctg ttg gag				1489
Arg Val Leu Ser Thr Leu Asn Val Leu Val Thr Pro Glu Leu Leu Glu				
	480	485	490	
aca ggt gtt gaa tgc acg gcc tcc aac gac ctg ggc aaa aac acc agc				1537
Thr Gly Val Glu Cys Thr Ala Ser Asn Asp Leu Gly Lys Asn Thr Ser				
495	500	505	510	
atc ctc ttc ctg gag ctg gtc aat tta acc acc ctc aca cca gac tcc				1585
Ile Leu Phe Leu Glu Leu Val Asn Leu Thr Thr Leu Thr Pro Asp Ser				
	515	520	525	
aac aca acc act ggc ctc agc act tcc act gcc agt cct cat acc aga				1633
Asn Thr Thr Thr Gly Leu Ser Thr Ser Thr Ala Ser Pro His Thr Arg				
	530	535	540	
gcc aac agc acc tcc aca gag aga aag ctg ccg gag ccg gag agc cgg				1681
Ala Asn Ser Thr Ser Thr Glu Arg Lys Leu Pro Glu Pro Glu Ser Arg				

PH-1064PCT-US seq.TXT

545	550	555	
ggc gtg gtc atc gtg gct gtg att gtg tgc atc ctg gtc ctg gcg gtg			1729
Gly Val Val Ile Val Ala Val Ile Val Cys Ile Leu Val Leu Ala Val			
560	565	570	
ctg ggc gct gtc ctc tat ttc ctc tat aag aag ggc aag ctg ccg tgc			1777
Leu Gly Ala Val Leu Tyr Phe Leu Tyr Lys Lys Gly Lys Leu Pro Cys			
575	580	585	590
agg cgc tca ggg aag cag gag atc acg ctg ccc ccg tct cgt aag acc			1825
Arg Arg Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr			
	595	600	605
gaa ctt gta gtt gaa gtt aag tca gat aag ctc cca gaa gag atg ggc			1873
Glu Leu Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly			
	610	615	620
ctc ctg cag ggc agc agc ggt gac aag agg gct ccg gga gac cag gga			1921
Leu Leu Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly			
	625	630	635
gag aaa tac atc gat ctg agg cat tagccccgaa tcacttcagc tcccttcct			1975
Glu Lys Tyr Ile Asp Leu Arg His			
640	645		
gcctggacca ttcccagctc cctgctcact cttctctcag ccaaagctca aagggactag			2035
agagaagcct cctgctcccc tcgctgcac accccctttc agagggccac tgggttagga			2095
cctgaggacc tcacttggcc ctgcaaggcc cgcttttcag ggaccagtcc accaccatct			2155
cctccacgtt gagtgaagct catcccaagc aaggagcccc agtctcccga gcgggtagga			2215
gagtttcttg cagaacgtgt tttttcttta cacacattat gctgtaaata cgctcgtcct			2275

PH-1064PCT-US seq.TXT

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tgcaagcttg catgcctgcg tgttgctgca ccaccctcct gtctgcctct tcaaagtctc 2515
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caciaagtca gacgagacca tcctggctaa cacggtgaaa ccctgtctct actaaaaata 2695
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gaagcaggag aatggtatga atccaggagg tggagcttgc agtgagccga gaccgtgcca 2815
ctgcactcca gcctgggcaa cacagcgaga ctccgtctcg aggaaaaaaaa aaatcgtgct 2875
cgtagcagct ggctctgttt cgagtcaggt gaattagcct caatccccgt gttcacttgc 2935
tcccatagcc ctcttgatgg atcacgtaaa actgaaaggc agcggggagc agacaaagat 2995
gaggtctaca ctgtccttca tggggattaa agctatggtt atattagcac caaacttcta 3055
caaaccaagc tcaggaccca accctagaag ggcccaaagt agagaatggt acttagggat 3115
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gtgtgtatat atgggtttgt cagggtgtgta aatttgcaaa ttgtttcctt tatatatgta 3235
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<210> 96

<211> 646

<212> PRT

<213> Homo sapiens

<400> 96

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PH-1064PCT-US seq.TXT

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Gly Leu Ser Gln Ser Gln Gly Asn Leu Ser His Val Asp Trp Phe Ser			
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Val His Lys Glu Lys Arg Thr Leu Ile Phe Arg Val Arg Gln Gly Gln			
65	70	75	80
Gly Gln Ser Glu Pro Gly Glu Tyr Glu Gln Arg Leu Ser Leu Gln Asp			
85	90	95	
Arg Gly Ala Thr Leu Ala Leu Thr Gln Val Thr Pro Gln Asp Glu Arg			
100	105	110	
Ile Phe Leu Cys Gln Gly Lys Arg Pro Arg Ser Gln Glu Tyr Arg Ile			
115	120	125	
Gln Leu Arg Val Tyr Lys Ala Pro Glu Glu Pro Asn Ile Gln Val Asn			
130	135	140	
Pro Leu Gly Ile Pro Val Asn Ser Lys Glu Pro Glu Glu Val Ala Thr			
145	150	155	160
Cys Val Gly Arg Asn Gly Tyr Pro Ile Pro Gln Val Ile Trp Tyr Lys			
165	170	175	
Asn Gly Arg Pro Leu Lys Glu Glu Lys Asn Arg Val His Ile Gln Ser			
180	185	190	
Ser Gln Thr Val Glu Ser Ser Gly Leu Tyr Thr Leu Gln Ser Ile Leu			

PH-1064PCT-US seq.TXT

195	200	205
Lys Ala Gln Leu Val Lys Glu Asp Lys Asp Ala Gln Phe Tyr Cys Glu		
210	215	220
Leu Asn Tyr Arg Leu Pro Ser Gly Asn His Met Lys Glu Ser Arg Glu		
225	230	235
Val Thr Val Pro Val Phe Tyr Pro Thr Glu Lys Val Trp Leu Glu Val		
245	250	255
Glu Pro Val Gly Met Leu Lys Glu Gly Asp Arg Val Glu Ile Arg Cys		
260	265	270
Leu Ala Asp Gly Asn Pro Pro Pro His Phe Ser Ile Ser Lys Gln Asn		
275	280	285
Pro Ser Thr Arg Glu Ala Glu Glu Glu Thr Thr Asn Asp Asn Gly Val		
290	295	300
Leu Val Leu Glu Pro Ala Arg Lys Glu His Ser Gly Arg Tyr Glu Cys		
305	310	315
Gln Ala Trp Asn Leu Asp Thr Met Ile Ser Leu Leu Ser Glu Pro Gln		
325	330	335
Glu Leu Leu Val Asn Tyr Val Ser Asp Val Arg Val Ser Pro Ala Ala		
340	345	350
Pro Glu Arg Gln Glu Gly Ser Ser Leu Thr Leu Thr Cys Glu Ala Glu		
355	360	365
Ser Ser Gln Asp Leu Glu Phe Gln Trp Leu Arg Glu Glu Thr Asp Gln		
370	375	380
Val Leu Glu Arg Gly Pro Val Leu Gln Leu His Asp Leu Lys Arg Glu		

PH-1064PCT-US seq.TXT

385		390		395		400
Ala	Gly	Gly	Gly	Tyr	Arg	Cys
		405			410	
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		420			425	
Met	Ala	Phe	Lys	Glu	Arg	Lys
		435			440	
Asn	Leu	Ser	Cys	Glu	Ala	Ser
		450			455	
Asn	Val	Asn	Gly	Thr	Ala	Ser
		465			470	
Leu	Ser	Thr	Leu	Asn	Val	Leu
		485			490	
Val	Glu	Cys	Thr	Ala	Ser	Asn
		500			505	
Phe	Leu	Glu	Leu	Val	Asn	Leu
		515			520	
Thr	Thr	Gly	Leu	Ser	Thr	Ser
		530			535	
Ser	Thr	Ser	Thr	Glu	Arg	Lys
		545			550	
Val	Ile	Val	Ala	Val	Ile	Val
		565			570	
Ala	Val	Leu	Tyr	Phe	Leu	Tyr

PH-1064PCT-US seq.TXT

580	585	590
Ser Gly Lys Gln Glu Ile Thr Leu Pro Pro Ser Arg Lys Thr Glu Leu		
595	600	605
Val Val Glu Val Lys Ser Asp Lys Leu Pro Glu Glu Met Gly Leu Leu		
610	615	620
Gln Gly Ser Ser Gly Asp Lys Arg Ala Pro Gly Asp Gln Gly Glu Lys		
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Tyr Ile Asp Leu Arg His		640
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<210> 97

<211> 1642

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (158)..(1279)

<400> 97

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 ctgacttttg aaatctcggt taaccttcaa actggcg atg tca agg gtt cca agt 175

Met Ser Arg Val Pro Ser

1

5

cct cca cct ccg gca gaa atg tcg agt ggc ccc gta gct gag agt tgg 223
 Pro Pro Pro Pro Ala Glu Met Ser Ser Gly Pro Val Ala Glu Ser Trp

PH-1064PCT-US seq.TXT

10	15	20	
tgc tac aca cag atc aag gta gtg aaa ttc tcc tac atg tgg acc atc	271		
Cys Tyr Thr Gln Ile Lys Val Val Lys Phe Ser Tyr Met Trp Thr Ile			
25	30	35	
aat aac ttt agc ttt tgc cgg gag gaa atg ggt gaa gtc att aaa agt	319		
Asn Asn Phe Ser Phe Cys Arg Glu Glu Met Gly Glu Val Ile Lys Ser			
40	45	50	
tct aca ttt tca tca gga gca aat gat aaa ctg aaa tgg tgt ttg cga	367		
Ser Thr Phe Ser Ser Gly Ala Asn Asp Lys Leu Lys Trp Cys Leu Arg			
55	60	65	70
gta aac ccc aaa ggg tta gat gaa gaa agc aaa gat tac ctg tca ctt	415		
Val Asn Pro Lys Gly Leu Asp Glu Glu Ser Lys Asp Tyr Leu Ser Leu			
75	80	85	
tac ctg tta ctg gtc agc tgt cca aag agt gaa gtt cgg gca aaa ttc	463		
Tyr Leu Leu Leu Val Ser Cys Pro Lys Ser Glu Val Arg Ala Lys Phe			
90	95	100	
aaa ttc tcc atc ctg aat gcc aag gga gaa gaa acc aaa gct atg gag	511		
Lys Phe Ser Ile Leu Asn Ala Lys Gly Glu Glu Thr Lys Ala Met Glu			
105	110	115	
agt caa cgg gca tat agg ttt gtg caa ggc aaa gac tgg gga ttc aag	559		
Ser Gln Arg Ala Tyr Arg Phe Val Gln Gly Lys Asp Trp Gly Phe Lys			
120	125	130	
aaa ttc atc cgt aga gat ttt ctt ttg gat gag gcc aac ggg ctt ctc	607		
Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp Glu Ala Asn Gly Leu Leu			

PH-1064PCT-US seq.TXT

135	140	145	150	
cct gat gac aag ctt acc ctc ttc tgc gag gtg agt gtt gtg caa gat	655			
Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu Val Ser Val Val Gln Asp				
155	160	165		
tct gtc aac att tct ggc cag aat acc atg aac atg gta aag gtt cct	703			
Ser Val Asn Ile Ser Gly Gln Asn Thr Met Asn Met Val Lys Val Pro				
170	175	180		
gag tgc cgg ctg gca gat gag tta gga gga ctg tgg gag aat tcc cgg	751			
Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly Leu Trp Glu Asn Ser Arg				
185	190	195		
ttc aca gac tgc tgc ttg tgt gtt gcc ggc cag gaa ttc cag gct cac	799			
Phe Thr Asp Cys Cys Leu Cys Val Ala Gly Gln Glu Phe Gln Ala His				
200	205	210		
aag gct atc tta gca gct cgt tct ccg gtt ttt agt gcc atg ttt gaa	847			
Lys Ala Ile Leu Ala Ala Arg Ser Pro Val Phe Ser Ala Met Phe Glu				
215	220	225	230	
cat gaa atg gag gag agc aaa aag aat cga gtt gaa atc aat gat gtg	895			
His Glu Met Glu Glu Ser Lys Lys Asn Arg Val Glu Ile Asn Asp Val				
235	240	245		
gag cct gaa gtt ttt aag gaa atg atg tgc ttc att tac acg ggg aag	943			
Glu Pro Glu Val Phe Lys Glu Met Met Cys Phe Ile Tyr Thr Gly Lys				
250	255	260		
gct cca aac ctc gac aaa atg gct gat gat ttg ctg gca gct gct gac	991			
Ala Pro Asn Leu Asp Lys Met Ala Asp Asp Leu Leu Ala Ala Ala Asp				

PH-1064PCT-US seq.TXT

265	270	275	
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Lys Tyr Ala Leu Glu Arg Leu Lys Val Met Cys Glu Asp Ala Leu Cys			
280	285	290	
agt aac ctg tcc gtg gag aac gct gca gaa att ctc atc ctg gcc gac			1087
Ser Asn Leu Ser Val Glu Asn Ala Ala Glu Ile Leu Ile Leu Ala Asp			
295	300	305	310
ctc cac agt gca gat cag ttg aaa act cag gca gtg gat ttc atc aac			1135
Leu His Ser Ala Asp Gln Leu Lys Thr Gln Ala Val Asp Phe Ile Asn			
315	320	325	
tat cat gct tcg gat gtc ttg gag acc tct ggg tgg aag tca atg gtg			1183
Tyr His Ala Ser Asp Val Leu Glu Thr Ser Gly Trp Lys Ser Met Val			
330	335	340	
gtg tca cat ccc cac ttg gtg gct gag gca tac cgc tct ctg gct tca			1231
Val Ser His Pro His Leu Val Ala Glu Ala Tyr Arg Ser Leu Ala Ser			
345	350	355	
gca cag tgc cct ttt ctg gga ccc cca cgc aaa cgc ctg aag caa tcc			1279
Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg Lys Arg Leu Lys Gln Ser			
360	365	370	
taagatcctg cttgttgtaa gactccgttt aatttccaga agcagcagcc actgttgctg			1339
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gagggaaaat gaaatgaaaa ccctgttgct gcgtcactgt gttccctttg gcctgtctga			1519
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PH-1064PCT-US seq.TXT

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<210> 98

<211> 374

<212> PRT

<213> Homo sapiens

<400> 98

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			20					25					30		
Ser	Tyr	Met	Trp	Thr	Ile	Asn	Asn	Phe	Ser	Phe	Cys	Arg	Glu	Glu	Met
		35				40					45				
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	50					55					60				
Leu	Lys	Trp	Cys	Leu	Arg	Val	Asn	Pro	Lys	Gly	Leu	Asp	Glu	Glu	Ser
65				70					75					80	
Lys	Asp	Tyr	Leu	Ser	Leu	Tyr	Leu	Leu	Leu	Val	Ser	Cys	Pro	Lys	Ser
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PH-1064PCT-US seq.TXT

Lys Asp Trp Gly Phe Lys Lys Phe Ile Arg Arg Asp Phe Leu Leu Asp
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 Glu Ala Asn Gly Leu Leu Pro Asp Asp Lys Leu Thr Leu Phe Cys Glu
 145 150 155 160
 Val Ser Val Val Gln Asp Ser Val Asn Ile Ser Gly Gln Asn Thr Met
 165 170 175
 Asn Met Val Lys Val Pro Glu Cys Arg Leu Ala Asp Glu Leu Gly Gly
 180 185 190
 Leu Trp Glu Asn Ser Arg Phe Thr Asp Cys Cys Leu Cys Val Ala Gly
 195 200 205
 Gln Glu Phe Gln Ala His Lys Ala Ile Leu Ala Ala Arg Ser Pro Val
 210 215 220
 Phe Ser Ala Met Phe Glu His Glu Met Glu Glu Ser Lys Lys Asn Arg
 225 230 235 240
 Val Glu Ile Asn Asp Val Glu Pro Glu Val Phe Lys Glu Met Met Cys
 245 250 255
 Phe Ile Tyr Thr Gly Lys Ala Pro Asn Leu Asp Lys Met Ala Asp Asp
 260 265 270
 Leu Leu Ala Ala Ala Asp Lys Tyr Ala Leu Glu Arg Leu Lys Val Met
 275 280 285
 Cys Glu Asp Ala Leu Cys Ser Asn Leu Ser Val Glu Asn Ala Ala Glu
 290 295 300
 Ile Leu Ile Leu Ala Asp Leu His Ser Ala Asp Gln Leu Lys Thr Gln
 305 310 315 320

PH-1064PCT-US seq.TXT

Ala Val Asp Phe Ile Asn Tyr His Ala Ser Asp Val Leu Glu Thr Ser

325

330

335

Gly Trp Lys Ser Met Val Val Ser His Pro His Leu Val Ala Glu Ala

340

345

350

Tyr Arg Ser Leu Ala Ser Ala Gln Cys Pro Phe Leu Gly Pro Pro Arg

355

360

365

Lys Arg Leu Lys Gln Ser

370

<210> 99

<211> 5722

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (112)..(3621)

<400> 99

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Met Gly

1

ctg gcc tgg gga cta ggc gtc ctg ttc ctg atg cat gtg tgt ggc acc 165

Leu Ala Trp Gly Leu Gly Val Leu Phe Leu Met His Val Cys Gly Thr

5

10

15

aac cgc att cca gag tct ggc gga gac aac agc gtg ttt gac atc ttt 213

PH-1064PCT-US seq.TXT

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Glu	Leu	Thr	Gly	Ala	Ala	Arg	Lys	Gly	Ser	Gly	Arg	Arg	Leu	Val	Lys		
	35				40					45					50		
ggc	ccc	gac	cct	tcc	agc	cca	gct	ttc	cgc	atc	gag	gat	gcc	aac	ctg	309	
Gly	Pro	Asp	Pro	Ser	Ser	Pro	Ala	Phe	Arg	Ile	Glu	Asp	Ala	Asn	Leu		
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atc	ccc	cct	gtg	cct	gat	gac	aag	ttc	caa	gac	ctg	gtg	gat	gct	gtg	357	
Ile	Pro	Pro	Val	Pro	Asp	Asp	Lys	Phe	Gln	Asp	Leu	Val	Asp	Ala	Val		
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cgg	gca	gaa	aag	ggt	ttc	ctc	ctt	ctg	gca	tcc	ctg	agg	cag	atg	aag	405	
Arg	Ala	Glu	Lys	Gly	Phe	Leu	Leu	Leu	Ala	Ser	Leu	Arg	Gln	Met	Lys		
		85						90						95			
aag	acc	cgg	ggc	acg	ctg	ctg	gcc	ctg	gag	cgg	aaa	gac	cac	tct	ggc	453	
Lys	Thr	Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Arg	Lys	Asp	His	Ser	Gly		
		100						105						110			
cag	gtc	ttc	agc	gtg	gtg	tcc	aat	ggc	aag	gcg	ggc	acc	ctg	gac	ctc	501	
Gln	Val	Phe	Ser	Val	Val	Ser	Asn	Gly	Lys	Ala	Gly	Thr	Leu	Asp	Leu		
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agc	ctg	acc	gtc	caa	gga	aag	cag	cac	gtg	gtg	tct	gtg	gaa	gaa	gct	549	
Ser	Leu	Thr	Val	Gln	Gly	Lys	Gln	His	Val	Val	Ser	Val	Glu	Glu	Ala		
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ctc	ctg	gca	acc	ggc	cag	tgg	aag	agc	atc	acc	ctg	ttt	gtg	cag	gaa	597	

PH-1064PCT-US seq.TXT

Leu	Leu	Ala	Thr	Gly	Gln	Trp	Lys	Ser	Ile	Thr	Leu	Phe	Val	Gln	Glu		
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gac	agg	gcc	cag	ctg	tac	atc	gac	tgt	gaa	aag	atg	gag	aat	gct	gag	645	
Asp	Arg	Ala	Gln	Leu	Tyr	Ile	Asp	Cys	Glu	Lys	Met	Glu	Asn	Ala	Glu		
			165					170					175				
ttg	gac	gtc	ccc	atc	caa	agc	gtc	ttc	acc	aga	gac	ctg	gcc	agc	atc	693	
Leu	Asp	Val	Pro	Ile	Gln	Ser	Val	Phe	Thr	Arg	Asp	Leu	Ala	Ser	Ile		
			180					185					190				
gcc	aga	ctc	cgc	atc	gca	aag	ggg	ggc	gtc	aat	gac	aat	ttc	cag	ggg	741	
Ala	Arg	Leu	Arg	Ile	Ala	Lys	Gly	Gly	Val	Asn	Asp	Asn	Phe	Gln	Gly		
			195					200					205		210		
gtg	ctg	cag	aat	gtg	agg	ttt	gtc	ttt	gga	acc	aca	cca	gaa	gac	atc	789	
Val	Leu	Gln	Asn	Val	Arg	Phe	Val	Phe	Gly	Thr	Thr	Pro	Glu	Asp	Ile		
							215				220			225			
ctc	agg	aac	aaa	ggc	tgc	tcc	agc	tct	acc	agt	gtc	ctc	ctc	acc	ctt	837	
Leu	Arg	Asn	Lys	Gly	Cys	Ser	Ser	Ser	Thr	Ser	Val	Leu	Leu	Thr	Leu		
			230					235					240				
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Asp	Asn	Asn	Val	Val	Asn	Gly	Ser	Ser	Pro	Ala	Ile	Arg	Thr	Asn	Tyr		
			245					250					255				
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Ile	Gly	His	Lys	Thr	Lys	Asp	Leu	Gln	Ala	Ile	Cys	Gly	Ile	Ser	Cys		
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Val	Thr	Thr	Leu	Gln	Asp	Ser	Ile	Arg	Lys	Val	Thr	Glu	Glu	Asn	Lys		
			295					300						305			
gag	ttg	gcc	aat	gag	ctg	agg	cgg	cct	ccc	cta	tgc	tat	cac	aac	gga	1077	
Glu	Leu	Ala	Asn	Glu	Leu	Arg	Arg	Pro	Pro	Leu	Cys	Tyr	His	Asn	Gly		
		310						315					320				
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		325						330					335				
tgt	cac	tgt	cag	aac	tca	gtt	acc	atc	tgc	aaa	aag	gtg	tcc	tgc	ccc	1173	
Cys	His	Cys	Gln	Asn	Ser	Val	Thr	Ile	Cys	Lys	Lys	Val	Ser	Cys	Pro		
		340						345					350				
atc	atg	ccc	tgc	tcc	aat	gcc	aca	gtt	cct	gat	gga	gaa	tgc	tgt	cct	1221	
Ile	Met	Pro	Cys	Ser	Asn	Ala	Thr	Val	Pro	Asp	Gly	Glu	Cys	Cys	Pro		
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cgc	tgt	tgg	ccc	agc	gac	tct	gcg	gac	gat	ggc	tgg	tct	cca	tgg	tcc	1269	
Arg	Cys	Trp	Pro	Ser	Asp	Ser	Ala	Asp	Asp	Gly	Trp	Ser	Pro	Trp	Ser		
			375					380					385				
gag	tgg	acc	tcc	tgt	tct	acg	agc	tgt	ggc	aat	gga	att	cag	cag	cgc	1317	
Glu	Trp	Thr	Ser	Cys	Ser	Thr	Ser	Cys	Gly	Asn	Gly	Ile	Gln	Gln	Arg		
			390					395					400				
ggc	cgc	tcc	tgc	gat	agc	ctc	aac	aac	cga	tgt	gag	ggc	tcc	tcg	gtc	1365	

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Gly	Arg	Ser	Cys	Asp	Ser	Leu	Asn	Asn	Arg	Cys	Glu	Gly	Ser	Ser	Val		
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Gln	Thr	Arg	Thr	Cys	His	Ile	Gln	Glu	Cys	Asp	Lys	Arg	Phe	Lys	Gln		
		420					425					430					
gat	ggt	ggc	tgg	agc	cac	tgg	tcc	ccg	tgg	tca	tct	tgt	tct	gtg	aca	1461	
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tgt	ggt	gat	ggt	gtg	atc	aca	agg	atc	cgg	ctc	tgc	aac	tct	ccc	agc	1509	
Cys	Gly	Asp	Gly	Val	Ile	Thr	Arg	Ile	Arg	Leu	Cys	Asn	Ser	Pro	Ser		
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ccc	cag	atg	aat	ggg	aaa	ccc	tgt	gaa	ggc	gaa	gcg	cgg	gag	acc	aaa	1557	
Pro	Gln	Met	Asn	Gly	Lys	Pro	Cys	Glu	Gly	Glu	Ala	Arg	Glu	Thr	Lys		
				470					475					480			
gcc	tgc	aag	aaa	gac	gcc	tgc	ccc	atc	aat	gga	ggc	tgg	ggt	cct	tgg	1605	
Ala	Cys	Lys	Lys	Asp	Ala	Cys	Pro	Ile	Asn	Gly	Gly	Trp	Gly	Pro	Trp		
		485					490					495					
tca	cca	tgg	gac	atc	tgt	tct	gtc	acc	tgt	gga	gga	ggg	gta	cag	aaa	1653	
Ser	Pro	Trp	Asp	Ile	Cys	Ser	Val	Thr	Cys	Gly	Gly	Gly	Val	Gln	Lys		
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cgt	agt	cgt	ctc	tgc	aac	aac	ccc	gca	ccc	cag	ttt	gga	ggc	aag	gac	1701	
Arg	Ser	Arg	Leu	Cys	Asn	Asn	Pro	Ala	Pro	Gln	Phe	Gly	Gly	Lys	Asp		
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Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln Asp Cys	
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cca att gat gga tgc ctg tcc aat ccc tgc ttt gcc ggc gtg aag tgt	1797
Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val Lys Cys	
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act agc tac cct gat ggc agc tgg aaa tgt ggt gct tgt ccc cct ggt	1845
Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro Pro Gly	
565	570
tac agt gga aat ggc atc cag tgc aca gat gtt gat gag tgc aaa gaa	1893
Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys Lys Glu	
580	585
gtg cct gat gcc tgc ttc aac cac aat gga gag cac cgg tgt gag aac	1941
Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys Glu Asn	
595	600
acg gac ccc ggc tac aac tgc ctg ccc tgc ccc cca cgc ttc acc ggc	1989
Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe Thr Gly	
615	620
tca cag ccc ttc ggc cag ggt gtc gaa cat gcc acg gcc aac aaa cag	2037
Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn Lys Gln	
630	635
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Val Cys Lys Pro Arg Asn Pro Cys Thr Asp Gly Thr His Asp Cys Asn	
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aag aac gcc aag tgc aac tac ctg ggc cac tat agc gac ccc atg tac	2133

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Arg	Cys	Glu	Cys	Lys	Pro	Gly	Tyr	Ala	Gly	Asn	Gly	Ile	Ile	Cys	Gly		
675					680					685					690		
gag	gac	aca	gac	ctg	gat	ggc	tgg	ccc	aat	gag	aac	ctg	gtg	tgc	gtg	2229	
Glu	Asp	Thr	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Glu	Asn	Leu	Val	Cys	Val		
				695					700					705			
gcc	aat	gcg	act	tac	cac	tgc	aaa	aag	gat	aat	tgc	ccc	aac	ctt	ccc	2277	
Ala	Asn	Ala	Thr	Tyr	His	Cys	Lys	Lys	Asp	Asn	Cys	Pro	Asn	Leu	Pro		
			710					715						720			
aac	tca	ggg	cag	gaa	gac	tat	gac	aag	gat	gga	att	ggt	gat	gcc	tgt	2325	
Asn	Ser	Gly	Gln	Glu	Asp	Tyr	Asp	Lys	Asp	Gly	Ile	Gly	Asp	Ala	Cys		
		725						730						735			
gat	gat	gac	gat	gac	aat	gat	aaa	att	cca	gat	gac	agg	gac	aac	tgt	2373	
Asp	Asp	Asp	Asp	Asp	Asn	Asp	Lys	Ile	Pro	Asp	Asp	Arg	Asp	Asn	Cys		
		740						745						750			
cca	ttc	cat	tac	aac	cca	gct	cag	tat	gac	tat	gac	aga	gat	gat	gtg	2421	
Pro	Phe	His	Tyr	Asn	Pro	Ala	Gln	Tyr	Asp	Tyr	Asp	Arg	Asp	Asp	Val		
755					760						765				770		
gga	gac	cgc	tgt	gac	aac	tgt	ccc	tac	aac	cac	aac	cca	gat	cag	gca	2469	
Gly	Asp	Arg	Cys	Asp	Asn	Cys	Pro	Tyr	Asn	His	Asn	Pro	Asp	Gln	Ala		
				775						780				785			
gac	aca	gac	aac	aat	ggg	gaa	gga	gac	gcc	tgt	gct	gca	gac	att	gat	2517	

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Asp Thr Asp Asn Asn Gly Glu Gly Asp Ala Cys Ala Ala Asp Ile Asp	
790	795
800	
gga gac ggt atc ctc aat gaa cgg gac aac tgc cag tac gtc tac aat	2565
Gly Asp Gly Ile Leu Asn Glu Arg Asp Asn Cys Gln Tyr Val Tyr Asn	
805	810
815	
gtg gac cag aga gac act gat atg gat ggg gtt gga gat cag tgt gac	2613
Val Asp Gln Arg Asp Thr Asp Met Asp Gly Val Gly Asp Gln Cys Asp	
820	825
830	
aat tgc ccc ttg gaa cac aat ccg gat cag ctg gac tct gac tca gac	2661
Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp Ser Asp	
835	840
845	850
cgc att gga gat acc tgt gac aac aat cag gat att gat gaa gat ggc	2709
Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu Asp Gly	
855	860
865	
cac cag aac aat ctg gac aac tgt ccc tat gtg ccc aat gcc aac cag	2757
His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala Asn Gln	
870	875
880	
gct gac cat gac aaa gat ggc aag gga gat gcc tgt gac cac gat gat	2805
Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His Asp Asp	
885	890
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gac aac gat ggc att cct gat gac aag gac aac tgc aga ctc gtg ccc	2853
Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu Val Pro	
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Asn	Pro	Asp	Gln	Lys	Asp	Ser	Asp	Gly	Asp	Gly	Arg	Gly	Asp	Ala	Cys		
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Lys	Asp	Asp	Phe	Asp	His	Asp	Ser	Val	Pro	Asp	Ile	Asp	Asp	Ile	Cys		
			935						940					945			
cct	gag	aat	gtt	gac	atc	agt	gag	acc	gat	ttc	cgc	cga	ttc	cag	atg	2997	
Pro	Glu	Asn	Val	Asp	Ile	Ser	Glu	Thr	Asp	Phe	Arg	Arg	Phe	Gln	Met		
			950						955					960			
att	cct	ctg	gac	ccc	aaa	ggg	aca	tcc	caa	aat	gac	cct	aac	tgg	gtt	3045	
Ile	Pro	Leu	Asp	Pro	Lys	Gly	Thr	Ser	Gln	Asn	Asp	Pro	Asn	Trp	Val		
			965						970					975			
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Val	Arg	His	Gln	Gly	Lys	Glu	Leu	Val	Gln	Thr	Val	Asn	Cys	Asp	Pro		
			980						985					990			
gga	ctc	gct	gta	ggt	tat	gat	gag	ttt	aat	gct	gtg	gac	ttc	agt	ggc	3141	
Gly	Leu	Ala	Val	Gly	Tyr	Asp	Glu	Phe	Asn	Ala	Val	Asp	Phe	Ser	Gly		
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acc	ttc	ttc	atc	aac	acc	gaa	agg	gac	gat	gac	tat	gct	gga	ttt	gtc	3189	
Thr	Phe	Phe	Ile	Asn	Thr	Glu	Arg	Asp	Asp	Asp	Tyr	Ala	Gly	Phe	Val		
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Phe	Gly	Tyr	Gln	Ser	Ser	Ser	Arg	Phe	Tyr	Val	Val	Met	Trp	Lys	Gln		
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cac ctg cgg aac gcc ctg tgg cac aca gga aac acc cct ggc cag gtg	3381
His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly Gln Val	
1075	1080
1085	1090
cgc acc ctg tgg cat gac cct cgt cac ata ggc tgg aaa gat ttc acc	3429
Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp Phe Thr	
1095	1100
1105	
gcc tac aga tgg cgt ctc agc cac agg cca aag acg ggt ttc att aga	3477
Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe Ile Arg	
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1120	
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Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly Pro Ile	
1125	1130
1135	
tat gat aaa acc tat gct ggt ggt aga cta ggg ttg ttt gtc ttc tct	3573
Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val Phe Ser	
1140	1145
1150	
caa gaa atg gtg ttc ttc tct gac ctg aaa tac gaa tgt aga gat ccc	3621
Gln Glu Met Val Phe Phe Ser Asp Leu Lys Tyr Glu Cys Arg Asp Pro	
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<211> 1170

<212> PRT

<213> Homo sapiens

<400> 100

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Gly	Thr	Asn	Arg	Ile	Pro	Glu	Ser	Gly	Gly	Asp	Asn	Ser	Val	Phe	Asp
				20					25					30	
Ile	Phe	Glu	Leu	Thr	Gly	Ala	Ala	Arg	Lys	Gly	Ser	Gly	Arg	Arg	Leu
		35						40					45		
Val	Lys	Gly	Pro	Asp	Pro	Ser	Ser	Pro	Ala	Phe	Arg	Ile	Glu	Asp	Ala

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Asn	Leu	Ile	Pro	Pro	Val	Pro	Asp	Asp	Lys	Phe	Gln	Asp	Leu	Val	Asp
65					70					75					80
Ala	Val	Arg	Ala	Glu	Lys	Gly	Phe	Leu	Leu	Leu	Ala	Ser	Leu	Arg	Gln
				85						90					95
Met	Lys	Lys	Thr	Arg	Gly	Thr	Leu	Leu	Ala	Leu	Glu	Arg	Lys	Asp	His
			100						105					110	
Ser	Gly	Gln	Val	Phe	Ser	Val	Val	Ser	Asn	Gly	Lys	Ala	Gly	Thr	Leu
		115							120					125	
Asp	Leu	Ser	Leu	Thr	Val	Gln	Gly	Lys	Gln	His	Val	Val	Ser	Val	Glu
	130					135							140		
Glu	Ala	Leu	Leu	Ala	Thr	Gly	Gln	Trp	Lys	Ser	Ile	Thr	Leu	Phe	Val
145				150						155					160
Gln	Glu	Asp	Arg	Ala	Gln	Leu	Tyr	Ile	Asp	Cys	Glu	Lys	Met	Glu	Asn
			165						170					175	
Ala	Glu	Leu	Asp	Val	Pro	Ile	Gln	Ser	Val	Phe	Thr	Arg	Asp	Leu	Ala
		180							185					190	
Ser	Ile	Ala	Arg	Leu	Arg	Ile	Ala	Lys	Gly	Gly	Val	Asn	Asp	Asn	Phe
	195							200					205		
Gln	Gly	Val	Leu	Gln	Asn	Val	Arg	Phe	Val	Phe	Gly	Thr	Thr	Pro	Glu
	210					215					220				
Asp	Ile	Leu	Arg	Asn	Lys	Gly	Cys	Ser	Ser	Ser	Thr	Ser	Val	Leu	Leu
225				230						235					240
Thr	Leu	Asp	Asn	Asn	Val	Val	Asn	Gly	Ser	Ser	Pro	Ala	Ile	Arg	Thr

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275	280	285
Thr Ile Val Thr Thr Leu Gln Asp Ser Ile Arg Lys Val Thr Glu Glu		
290	295	300
Asn Lys Glu Leu Ala Asn Glu Leu Arg Arg Pro Pro Leu Cys Tyr His		
305	310	315
Asn Gly Val Gln Tyr Arg Asn Asn Glu Glu Trp Thr Val Asp Ser Cys		
325	330	335
Thr Glu Cys His Cys Gln Asn Ser Val Thr Ile Cys Lys Lys Val Ser		
340	345	350
Cys Pro Ile Met Pro Cys Ser Asn Ala Thr Val Pro Asp Gly Glu Cys		
355	360	365
Cys Pro Arg Cys Trp Pro Ser Asp Ser Ala Asp Asp Gly Trp Ser Pro		
370	375	380
Trp Ser Glu Trp Thr Ser Cys Ser Thr Ser Cys Gly Asn Gly Ile Gln		
385	390	395
Gln Arg Gly Arg Ser Cys Asp Ser Leu Asn Asn Arg Cys Glu Gly Ser		
405	410	415
Ser Val Gln Thr Arg Thr Cys His Ile Gln Glu Cys Asp Lys Arg Phe		
420	425	430
Lys Gln Asp Gly Gly Trp Ser His Trp Ser Pro Trp Ser Ser Cys Ser		

PH-1064PCT-US seq.TXT

435		440		445
Val Thr Cys Gly Asp Gly Val Ile Thr Arg Ile Arg Leu Cys Asn Ser				
450		455		460
Pro Ser Pro Gln Met Asn Gly Lys Pro Cys Glu Gly Glu Ala Arg Glu				
465		470		475
Thr Lys Ala Cys Lys Lys Asp Ala Cys Pro Ile Asn Gly Gly Trp Gly				
	485		490	
Pro Trp Ser Pro Trp Asp Ile Cys Ser Val Thr Cys Gly Gly Gly Val				
	500		505	
Gln Lys Arg Ser Arg Leu Cys Asn Asn Pro Ala Pro Gln Phe Gly Gly				
	515		520	
Lys Asp Cys Val Gly Asp Val Thr Glu Asn Gln Ile Cys Asn Lys Gln				
	530		535	
Asp Cys Pro Ile Asp Gly Cys Leu Ser Asn Pro Cys Phe Ala Gly Val				
545		550		555
Lys Cys Thr Ser Tyr Pro Asp Gly Ser Trp Lys Cys Gly Ala Cys Pro				
	565		570	
Pro Gly Tyr Ser Gly Asn Gly Ile Gln Cys Thr Asp Val Asp Glu Cys				
	580		585	
Lys Glu Val Pro Asp Ala Cys Phe Asn His Asn Gly Glu His Arg Cys				
	595		600	
Glu Asn Thr Asp Pro Gly Tyr Asn Cys Leu Pro Cys Pro Pro Arg Phe				
	610		615	
Thr Gly Ser Gln Pro Phe Gly Gln Gly Val Glu His Ala Thr Ala Asn				

PH-1064PCT-US seq.TXT

625		630		635		640									
Lys	Gln	Val	Cys	Lys	Pro	Arg	Asn	Pro	Cys	Thr	Asp	Gly	Thr	His	Asp
				645					650					655	
Cys	Asn	Lys	Asn	Ala	Lys	Cys	Asn	Tyr	Leu	Gly	His	Tyr	Ser	Asp	Pro
				660					665					670	
Met	Tyr	Arg	Cys	Glu	Cys	Lys	Pro	Gly	Tyr	Ala	Gly	Asn	Gly	Ile	Ile
				675					680					685	
Cys	Gly	Glu	Asp	Thr	Asp	Leu	Asp	Gly	Trp	Pro	Asn	Glu	Asn	Leu	Val
				690					695					700	
Cys	Val	Ala	Asn	Ala	Thr	Tyr	His	Cys	Lys	Lys	Asp	Asn	Cys	Pro	Asn
705									710					715	
Leu	Pro	Asn	Ser	Gly	Gln	Glu	Asp	Tyr	Asp	Lys	Asp	Gly	Ile	Gly	Asp
									725					730	
Ala	Cys	Asp	Asp	Asp	Asp	Asp	Asn	Asp	Lys	Ile	Pro	Asp	Asp	Arg	Asp
									740					745	
Asn	Cys	Pro	Phe	His	Tyr	Asn	Pro	Ala	Gln	Tyr	Asp	Tyr	Asp	Arg	Asp
									755					760	
Asp	Val	Gly	Asp	Arg	Cys	Asp	Asn	Cys	Pro	Tyr	Asn	His	Asn	Pro	Asp
									770					775	
Gln	Ala	Asp	Thr	Asp	Asn	Asn	Gly	Glu	Gly	Asp	Ala	Cys	Ala	Ala	Asp
									785					790	
Ile	Asp	Gly	Asp	Gly	Ile	Leu	Asn	Glu	Arg	Asp	Asn	Cys	Gln	Tyr	Val
									805					810	
Tyr	Asn	Val	Asp	Gln	Arg	Asp	Thr	Asp	Met	Asp	Gly	Val	Gly	Asp	Gln

PH-1064PCT-US seq.TXT

820		825		830
Cys Asp Asn Cys Pro Leu Glu His Asn Pro Asp Gln Leu Asp Ser Asp				
835		840		845
Ser Asp Arg Ile Gly Asp Thr Cys Asp Asn Asn Gln Asp Ile Asp Glu				
850		855		860
Asp Gly His Gln Asn Asn Leu Asp Asn Cys Pro Tyr Val Pro Asn Ala				
865		870		875
Asn Gln Ala Asp His Asp Lys Asp Gly Lys Gly Asp Ala Cys Asp His				
	885		890	
Asp Asp Asp Asn Asp Gly Ile Pro Asp Asp Lys Asp Asn Cys Arg Leu				
	900		905	
Val Pro Asn Pro Asp Gln Lys Asp Ser Asp Gly Asp Gly Arg Gly Asp				
	915		920	
Ala Cys Lys Asp Asp Phe Asp His Asp Ser Val Pro Asp Ile Asp Asp				
	930		935	
Ile Cys Pro Glu Asn Val Asp Ile Ser Glu Thr Asp Phe Arg Arg Phe				
945		950		955
Gln Met Ile Pro Leu Asp Pro Lys Gly Thr Ser Gln Asn Asp Pro Asn				
	965		970	
Trp Val Val Arg His Gln Gly Lys Glu Leu Val Gln Thr Val Asn Cys				
	980		985	
Asp Pro Gly Leu Ala Val Gly Tyr Asp Glu Phe Asn Ala Val Asp Phe				
	995		1000	
Ser Gly Thr Phe Phe Ile Asn Thr Glu Arg Asp Asp Asp Tyr Ala Gly				

PH-1064PCT-US seq.TXT

1010	1015	1020
Phe Val Phe Gly Tyr Gln Ser Ser Ser Arg Phe Tyr Val Val Met Trp		
1025	1030	1035
Lys Gln Val Thr Gln Ser Tyr Trp Asp Thr Asn Pro Thr Arg Ala Gln		
	1045	1050
		1055
Gly Tyr Ser Gly Leu Ser Val Lys Val Val Asn Ser Thr Thr Gly Pro		
	1060	1065
		1070
Gly Glu His Leu Arg Asn Ala Leu Trp His Thr Gly Asn Thr Pro Gly		
	1075	1080
		1085
Gln Val Arg Thr Leu Trp His Asp Pro Arg His Ile Gly Trp Lys Asp		
	1090	1095
		1100
Phe Thr Ala Tyr Arg Trp Arg Leu Ser His Arg Pro Lys Thr Gly Phe		
1105	1110	1115
		1120
Ile Arg Val Val Met Tyr Glu Gly Lys Lys Ile Met Ala Asp Ser Gly		
	1125	1130
		1135
Pro Ile Tyr Asp Lys Thr Tyr Ala Gly Gly Arg Leu Gly Leu Phe Val		
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Asp Pro		
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<211> 838

<212> DNA

PH-1064PCT-US seq.TXT

<213> Homo sapiens

<220>

<221> CDS

<222> (35)..(568)

<400> 101

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gac tcg gag gga cat ctc tac acc gtt ccc atc cgg gaa cag ggc aac 103

Asp Ser Glu Gly His Leu Tyr Thr Val Pro Ile Arg Glu Gln Gly Asn

10

15

20

atc tac aag ccc aac aac aag gcc atg gca gac gag ctg agc gag aag 151

Ile Tyr Lys Pro Asn Asn Lys Ala Met Ala Asp Glu Leu Ser Glu Lys

25

30

35

caa gtg tac gac gcg cac acc aag gag atc gac ctg gtc aac cgc gac 199

Gln Val Tyr Asp Ala His Thr Lys Glu Ile Asp Leu Val Asn Arg Asp

40

45

50

55

cct aaa cac ctc aac gat gac gtg gtc aag att gac ttt gaa gat gtg 247

Pro Lys His Leu Asn Asp Asp Val Val Lys Ile Asp Phe Glu Asp Val

60

65

70

att gca gaa cca gaa ggg aca cac agt ttt cac ggc att tgg aag gcc 295

Ile Ala Glu Pro Glu Gly Thr His Ser Phe His Gly Ile Trp Lys Ala

75

80

85

agc ttc acc acc ttc act gtg acg aaa tac tgg ttt tac cgc ttg ctg 343

PH-1064PCT-US seq.TXT

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Ser Ala Leu Phe Gly Ile Pro Met Ala Leu Ile Trp Gly Ile Tyr Phe
      105                      110                      115
gcc att ctc tct ttc ctg cac atc tgg gca gtt gta cca tgc att aag 439
Ala Ile Leu Ser Phe Leu His Ile Trp Ala Val Val Pro Cys Ile Lys
      120                      125                      130                      135
agc ttc ctg att gag att cag tgc acc agc cgt gtc tat tcc atc tac 487
Ser Phe Leu Ile Glu Ile Gln Cys Thr Ser Arg Val Tyr Ser Ile Tyr
      140                      145                      150
gtc cac acc gtc tgt gac cca ctc ttt gaa gct gtt ggg aaa ata ttc 535
Val His Thr Val Cys Asp Pro Leu Phe Glu Ala Val Gly Lys Ile Phe
      155                      160                      165
agc aat gtc cgc atc aac ttg cag aaa gaa ata taaatgacat ttcaaggata 588
Ser Asn Val Arg Ile Asn Leu Gln Lys Glu Ile
      170                      175
gaagtatacc tgattttttt tccttttaat tttcctggtg ccaatttcaa gttccaagtt 648
gctaatacag caacgaattt atgaattgaa ttatcttggt tgaaaataaa aagatcactt 708
tctcagtttt cataagtatt atgtctcttc tgagctatatt catctatttt tggcagtctg 768
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<210> 102

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PH-1064PCT-US seq.TXT

<211> 178

<212> PRT

<213> Homo sapiens

<400> 102

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			20					25					30		
Ala	Asp	Glu	Leu	Ser	Glu	Lys	Gln	Val	Tyr	Asp	Ala	His	Thr	Lys	Glu
		35					40					45			
Ile	Asp	Leu	Val	Asn	Arg	Asp	Pro	Lys	His	Leu	Asn	Asp	Asp	Val	Val
	50					55					60				
Lys	Ile	Asp	Phe	Glu	Asp	Val	Ile	Ala	Glu	Pro	Glu	Gly	Thr	His	Ser
65				70						75				80	
Phe	His	Gly	Ile	Trp	Lys	Ala	Ser	Phe	Thr	Thr	Phe	Thr	Val	Thr	Lys
			85						90				95		
Tyr	Trp	Phe	Tyr	Arg	Leu	Leu	Ser	Ala	Leu	Phe	Gly	Ile	Pro	Met	Ala
		100						105					110		
Leu	Ile	Trp	Gly	Ile	Tyr	Phe	Ala	Ile	Leu	Ser	Phe	Leu	His	Ile	Trp
		115					120					125			
Ala	Val	Val	Pro	Cys	Ile	Lys	Ser	Phe	Leu	Ile	Glu	Ile	Gln	Cys	Thr
	130					135					140				
Ser	Arg	Val	Tyr	Ser	Ile	Tyr	Val	His	Thr	Val	Cys	Asp	Pro	Leu	Phe
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PH-1064PCT-US seq.TXT

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165

170

175

Glu Ile

<210> 103

<211> 2269

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(444)

<400> 103

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Leu Phe Leu Thr Ile Pro Phe Ala Phe Phe Leu Pro Glu Leu Ile Phe	
20 25 30	
ggg ttc ttg gtc tgg acc atg gta gcc gcc acc cac ata gta tac ccc	144
Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro	
35 40 45	
ttg ctg caa gga tgg gtg atg tat gtc tcg ctc acc tcg ttt ctc atc	192
Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile	
50 55 60	
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PH-1064PCT-US seq.TXT

Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe
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gaa tcc tgg aga gtt ctg gac agc ctg tac cac ggg acc act ggc atc 288
Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile
85 90 95
ctg tac atg agc gct gcc gtc cta caa gta cat gcc acg att gtt tct 336
Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser
100 105 110
gag aaa ctg ctg gac cca aga att tac tac att aat tcg gca gcc tcg 384
Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser
115 120 125
ttc ttc gcc ttc atc gcc acg ctg ctc tac att ctc cat gcc ttc agc 432
Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser
130 135 140
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Ile Tyr Tyr His
145
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PH-1064PCT-US seq.TXT

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 aatttagttg tatttttagt agagatgggg tttcaccgta ttagccagga tggctctgat 1084
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PH-1064PCT-US seq.TXT

<210> 104

<211> 148

<212> PRT

<213> Homo sapiens

<400> 104

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          20              25              30
Gly Phe Leu Val Trp Thr Met Val Ala Ala Thr His Ile Val Tyr Pro
          35              40              45
Leu Leu Gln Gly Trp Val Met Tyr Val Ser Leu Thr Ser Phe Leu Ile
          50              55              60
Ser Leu Met Phe Leu Leu Ser Tyr Leu Phe Gly Phe Tyr Lys Arg Phe
  65              70              75              80
Glu Ser Trp Arg Val Leu Asp Ser Leu Tyr His Gly Thr Thr Gly Ile
          85              90              95
Leu Tyr Met Ser Ala Ala Val Leu Gln Val His Ala Thr Ile Val Ser
          100             105             110
Glu Lys Leu Leu Asp Pro Arg Ile Tyr Tyr Ile Asn Ser Ala Ala Ser
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Phe Phe Ala Phe Ile Ala Thr Leu Leu Tyr Ile Leu His Ala Phe Ser
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PH-1064PCT-US seq.TXT

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<211> 2899

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (91)..(2196)

<400> 105

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Met Ala Ala Pro Met Thr Pro Ala

1

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gct cgg ccc gag gac tac gag gcg gcg ctc aat gcc gcc ctg gct gac 162
Ala Arg Pro Glu Asp Tyr Glu Ala Ala Leu Asn Ala Ala Leu Ala Asp

10

15

20

gtg ccc gaa ctg gcc aga ctc ctg gag atc gac ccg tac ttg aag ccc 210
Val Pro Glu Leu Ala Arg Leu Leu Glu Ile Asp Pro Tyr Leu Lys Pro

25

30

35

40

tac gcc gtg gac ttc cag cgc agg tat aag cag ttt agc caa att ttg 258
Tyr Ala Val Asp Phe Gln Arg Arg Tyr Lys Gln Phe Ser Gln Ile Leu

45

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55

aag aac att gga gaa aat gaa ggt ggt att gat aag ttt tcc aga ggc 306
Lys Asn Ile Gly Glu Asn Glu Gly Gly Ile Asp Lys Phe Ser Arg Gly

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Tyr Glu Ser Phe Gly Val His Arg Cys Ala Asp Gly Gly Leu Tyr Ser			
75	80	85	
aaa gaa tgg gcc ccg gga gca gaa gga gtt ttt ctt act gga gat ttt			402
Lys Glu Trp Ala Pro Gly Ala Glu Gly Val Phe Leu Thr Gly Asp Phe			
90	95	100	
aat ggt tgg aat cca ttt tcg tac cca tac aaa aaa ctg gat tat gga			450
Asn Gly Trp Asn Pro Phe Ser Tyr Pro Tyr Lys Lys Leu Asp Tyr Gly			
105	110	115	120
aaa tgg gag ctg tat atc cca cca aag cag aat aaa tct gta ctc gtg			498
Lys Trp Glu Leu Tyr Ile Pro Pro Lys Gln Asn Lys Ser Val Leu Val			
125	130	135	
cct cat gga tcc aaa tta aag gta gtt att act agt aaa agc gga gag			546
Pro His Gly Ser Lys Leu Lys Val Val Ile Thr Ser Lys Ser Gly Glu			
140	145	150	
atc ttg tat cgt att tca ccg tgg gca aag tat gtg gtt cgt gaa ggt			594
Ile Leu Tyr Arg Ile Ser Pro Trp Ala Lys Tyr Val Val Arg Glu Gly			
155	160	165	
gat aat gtg aat tat gat tgg ata cac tgg gat cca gaa cac tca tat			642
Asp Asn Val Asn Tyr Asp Trp Ile His Trp Asp Pro Glu His Ser Tyr			
170	175	180	
gag ttt aag cat tcc aga cca aag aag cca cgg agt cta aga att tat			690
Glu Phe Lys His Ser Arg Pro Lys Lys Pro Arg Ser Leu Arg Ile Tyr			

PH-1064PCT-US seq.TXT

185	190	195	200	
gaa tct cat gtg gga att tct tcc cat gaa gga aaa gta gct tct tat				738
Glu Ser His Val Gly Ile Ser Ser His Glu Gly Lys Val Ala Ser Tyr				
	205	210	215	
aaa cat ttt aca tgc aat gta cta cca aga atc aaa ggc ctt gga tac				786
Lys His Phe Thr Cys Asn Val Leu Pro Arg Ile Lys Gly Leu Gly Tyr				
	220	225	230	
aac tgc att cag ttg atg gca atc atg gag cat gct tac tat gcc agc				834
Asn Cys Ile Gln Leu Met Ala Ile Met Glu His Ala Tyr Tyr Ala Ser				
	235	240	245	
ttt ggt tac caa atc aca agc ttc ttt gca gct tcc agc cgt tat gga				882
Phe Gly Tyr Gln Ile Thr Ser Phe Phe Ala Ala Ser Ser Arg Tyr Gly				
	250	255	260	
aca cct gaa gag cta caa gaa ctg gta gac aca gct cat tcc atg ggt				930
Thr Pro Glu Glu Leu Gln Glu Leu Val Asp Thr Ala His Ser Met Gly				
	265	270	275	280
atc ata gtc ctc tta gat gtg gta cac agc cat gct tca aaa aat tca				978
Ile Ile Val Leu Leu Asp Val Val His Ser His Ala Ser Lys Asn Ser				
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gca gat gga ttg aat atg ttt gat ggg aca gat tcc tgt tat ttt cat				1026
Ala Asp Gly Leu Asn Met Phe Asp Gly Thr Asp Ser Cys Tyr Phe His				
	300	305	310	
tct gga cct aga ggg act cat gat ctt tgg gat agc aga ttg ttt gcc				1074
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330	335	340	
tgg ttg gaa gaa tat cgc ttt gat gga ttt cgt ttt gat ggt gtt acg	1170		
Trp Leu Glu Glu Tyr Arg Phe Asp Gly Phe Arg Phe Asp Gly Val Thr			
345	350	355	360
tcc atg ctt tat cat cac cat gga gtg ggt caa ggt ttc tca ggt gat	1218		
Ser Met Leu Tyr His His His Gly Val Gly Gln Gly Phe Ser Gly Asp			
365	370	375	
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Tyr Ser Glu Tyr Phe Gly Leu Gln Val Asp Glu Asp Ala Leu Thr Tyr			
380	385	390	
ctc atg ttg gca aat cat ttg gtt cac acg ctg tgt ccc gat tct ata	1314		
Leu Met Leu Ala Asn His Leu Val His Thr Leu Cys Pro Asp Ser Ile			
395	400	405	
aca ata gct gag gat gta tca gga atg cca gct ctg tgc tct cca att	1362		
Thr Ile Ala Glu Asp Val Ser Gly Met Pro Ala Leu Cys Ser Pro Ile			
410	415	420	
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Ser Gln Gly Gly Gly Gly Phe Asp Tyr Arg Leu Ala Met Ala Ile Pro			
425	430	435	440
gat aag tgg att cag cta ctt aaa gag ttt aaa gat gaa gac tgg aac	1458		
Asp Lys Trp Ile Gln Leu Leu Lys Glu Phe Lys Asp Glu Asp Trp Asn			

PH-1064PCT-US seq.TXT

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460	465	470	
tgc att gct tat gca gag agc cat gat cag gca ttg gtt ggg gat aag	1554		
Cys Ile Ala Tyr Ala Glu Ser His Asp Gln Ala Leu Val Gly Asp Lys			
475	480	485	
tcg ctg gca ttt tgg ttg atg gat gcc gaa atg tat aca aac atg agt	1602		
Ser Leu Ala Phe Trp Leu Met Asp Ala Glu Met Tyr Thr Asn Met Ser			
490	495	500	
gtc ctg act cct ttt act cca gtt att gat cgt gga ata cag ctt cat	1650		
Val Leu Thr Pro Phe Thr Pro Val Ile Asp Arg Gly Ile Gln Leu His			
505	510	515	520
aaa atg att cga ctc att acg cat ggg ctt ggt gga gaa ggc tat ctc	1698		
Lys Met Ile Arg Leu Ile Thr His Gly Leu Gly Gly Glu Gly Tyr Leu			
525	530	535	
aat ttc atg ggt aat gaa ttt ggg cat cct gaa tgg tta gac ttc cca	1746		
Asn Phe Met Gly Asn Glu Phe Gly His Pro Glu Trp Leu Asp Phe Pro			
540	545	550	
aga aaa gga aat aat gag agt tac cat tat gcc agg cgg cag ttt cat	1794		
Arg Lys Gly Asn Asn Glu Ser Tyr His Tyr Ala Arg Arg Gln Phe His			
555	560	565	
tta act gac gac gac ctt ctt cgc tac aag ttc cta aat aat ttt gac	1842		
Leu Thr Asp Asp Asp Leu Leu Arg Tyr Lys Phe Leu Asn Asn Phe Asp			

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570	575	580	
agg gat atg aat aga ttg gaa gaa aga tat ggt tgg ctt gca gct cca	1890		
Arg Asp Met Asn Arg Leu Glu Glu Arg Tyr Gly Trp Leu Ala Ala Pro			
585	590	595	600
cag gcc tac gtg agt gaa aaa cat gaa ggc aat aag atc att gct ttt	1938		
Gln Ala Tyr Val Ser Glu Lys His Glu Gly Asn Lys Ile Ile Ala Phe			
605	610	615	
gaa aga gca ggt ctt ctt ttc att ttc aac ttc cat cca agc aag agc	1986		
Glu Arg Ala Gly Leu Leu Phe Ile Phe Asn Phe His Pro Ser Lys Ser			
620	625	630	
tac act gac tac cga gtt gga aca gca ttg cca ggg aaa ttc aaa att	2034		
Tyr Thr Asp Tyr Arg Val Gly Thr Ala Leu Pro Gly Lys Phe Lys Ile			
635	640	645	
gtg cta gat tca gat gca gcg gaa tat gga ggg cat cag aga ctg gac	2082		
Val Leu Asp Ser Asp Ala Ala Glu Tyr Gly Gly His Gln Arg Leu Asp			
650	655	660	
cac agc act gac ttt ttt tct gag gct ttt gaa cat aat ggg cgt ccc	2130		
His Ser Thr Asp Phe Phe Ser Glu Ala Phe Glu His Asn Gly Arg Pro			
665	670	675	680
tat tct ctt ttg gtg tac att cca agc aga gtg gcc ctc atc ctt cag	2178		
Tyr Ser Leu Leu Val Tyr Ile Pro Ser Arg Val Ala Leu Ile Leu Gln			
685	690	695	
aat gtg gat ctg ccg aat tgaagaggcc tgatttcagc tccaccagat	2226		
Asn Val Asp Leu Pro Asn			

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700

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<210> 106

<211> 702

<212> PRT

<213> Homo sapiens

<400> 106

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				20					25					30	
Glu	Ile	Asp	Pro	Tyr	Leu	Lys	Pro	Tyr	Ala	Val	Asp	Phe	Gln	Arg	Arg

PH-1064PCT-US seq.TXT

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Gly Ile Asp Lys Phe Ser Arg Gly Tyr Glu Ser Phe Gly Val His Arg		
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Cys Ala Asp Gly Gly Leu Tyr Ser Lys Glu Trp Ala Pro Gly Ala Glu		
85	90	95
Gly Val Phe Leu Thr Gly Asp Phe Asn Gly Trp Asn Pro Phe Ser Tyr		
100	105	110
Pro Tyr Lys Lys Leu Asp Tyr Gly Lys Trp Glu Leu Tyr Ile Pro Pro		
115	120	125
Lys Gln Asn Lys Ser Val Leu Val Pro His Gly Ser Lys Leu Lys Val		
130	135	140
Val Ile Thr Ser Lys Ser Gly Glu Ile Leu Tyr Arg Ile Ser Pro Trp		
145	150	155
Ala Lys Tyr Val Val Arg Glu Gly Asp Asn Val Asn Tyr Asp Trp Ile		
165	170	175
His Trp Asp Pro Glu His Ser Tyr Glu Phe Lys His Ser Arg Pro Lys		
180	185	190
Lys Pro Arg Ser Leu Arg Ile Tyr Glu Ser His Val Gly Ile Ser Ser		
195	200	205
His Glu Gly Lys Val Ala Ser Tyr Lys His Phe Thr Cys Asn Val Leu		
210	215	220
Pro Arg Ile Lys Gly Leu Gly Tyr Asn Cys Ile Gln Leu Met Ala Ile		

PH-1064PCT-US seq.TXT

225	230	235	240
Met Glu His Ala Tyr Tyr Ala Ser Phe Gly Tyr Gln Ile Thr Ser Phe			
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Phe Ala Ala Ser Ser Arg Tyr Gly Thr Pro Glu Glu Leu Gln Glu Leu			
	260	265	270
Val Asp Thr Ala His Ser Met Gly Ile Ile Val Leu Leu Asp Val Val			
	275	280	285
His Ser His Ala Ser Lys Asn Ser Ala Asp Gly Leu Asn Met Phe Asp			
	290	295	300
Gly Thr Asp Ser Cys Tyr Phe His Ser Gly Pro Arg Gly Thr His Asp			
305	310	315	320
Leu Trp Asp Ser Arg Leu Phe Ala Tyr Ser Ser Trp Glu Val Leu Arg			
	325	330	335
Phe Leu Leu Ser Asn Ile Arg Trp Trp Leu Glu Glu Tyr Arg Phe Asp			
	340	345	350
Gly Phe Arg Phe Asp Gly Val Thr Ser Met Leu Tyr His His His Gly			
	355	360	365
Val Gly Gln Gly Phe Ser Gly Asp Tyr Ser Glu Tyr Phe Gly Leu Gln			
	370	375	380
Val Asp Glu Asp Ala Leu Thr Tyr Leu Met Leu Ala Asn His Leu Val			
385	390	395	400
His Thr Leu Cys Pro Asp Ser Ile Thr Ile Ala Glu Asp Val Ser Gly			
	405	410	415
Met Pro Ala Leu Cys Ser Pro Ile Ser Gln Gly Gly Gly Gly Phe Asp			

PH-1064PCT-US seq.TXT

420	425	430
Tyr Arg Leu Ala Met Ala Ile Pro Asp Lys Trp Ile Gln Leu Leu Lys		
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Glu Phe Lys Asp Glu Asp Trp Asn Met Gly Asp Ile Val Tyr Thr Leu		
450	455	460
Thr Asn Arg Arg Tyr Leu Glu Lys Cys Ile Ala Tyr Ala Glu Ser His		
465	470	475
Asp Gln Ala Leu Val Gly Asp Lys Ser Leu Ala Phe Trp Leu Met Asp		
485	490	495
Ala Glu Met Tyr Thr Asn Met Ser Val Leu Thr Pro Phe Thr Pro Val		
500	505	510
Ile Asp Arg Gly Ile Gln Leu His Lys Met Ile Arg Leu Ile Thr His		
515	520	525
Gly Leu Gly Gly Glu Gly Tyr Leu Asn Phe Met Gly Asn Glu Phe Gly		
530	535	540
His Pro Glu Trp Leu Asp Phe Pro Arg Lys Gly Asn Asn Glu Ser Tyr		
545	550	555
His Tyr Ala Arg Arg Gln Phe His Leu Thr Asp Asp Asp Leu Leu Arg		
565	570	575
Tyr Lys Phe Leu Asn Asn Phe Asp Arg Asp Met Asn Arg Leu Glu Glu		
580	585	590
Arg Tyr Gly Trp Leu Ala Ala Pro Gln Ala Tyr Val Ser Glu Lys His		
595	600	605
Glu Gly Asn Lys Ile Ile Ala Phe Glu Arg Ala Gly Leu Leu Phe Ile		

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610

615

620

Phe Asn Phe His Pro Ser Lys Ser Tyr Thr Asp Tyr Arg Val Gly Thr

625

630

635

640

Ala Leu Pro Gly Lys Phe Lys Ile Val Leu Asp Ser Asp Ala Ala Glu

645

650

655

Tyr Gly Gly His Gln Arg Leu Asp His Ser Thr Asp Phe Phe Ser Glu

660

665

670

Ala Phe Glu His Asn Gly Arg Pro Tyr Ser Leu Leu Val Tyr Ile Pro

675

680

685

Ser Arg Val Ala Leu Ile Leu Gln Asn Val Asp Leu Pro Asn

690

695

700

<210> 107

<211> 790

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (78)..(626)

<400> 107

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Met Thr Thr Ala Ser Thr Ser Gln Val Arg Gln

1

5

10

aac tac cac cag gac tca gag gcc gcc atc aac cgc cag atc aac ctg 158

PH-1064PCT-US seq.TXT

Asn Tyr His Gln Asp Ser Glu Ala Ala Ile Asn Arg Gln Ile Asn Leu	
15 20 25	
gag ctc tac gcc tcc tac gtt tac ctg tcc atg tct tac tac ttt gac	206
Glu Leu Tyr Ala Ser Tyr Val Tyr Leu Ser Met Ser Tyr Tyr Phe Asp	
30 35 40	
cgc gat gat gtg gct ttg aag aac ttt gcc aaa tac ttt ctt cac caa	254
Arg Asp Asp Val Ala Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln	
45 50 55	
tct cat gag gag agg gaa cat gct gag aaa ctg atg aag ctg cag aac	302
Ser His Glu Glu Arg Glu His Ala Glu Lys Leu Met Lys Leu Gln Asn	
60 65 70 75	
caa cga ggt ggc cga atc ttc ctt cag gat atc aag aaa cca gac tgt	350
Gln Arg Gly Gly Arg Ile Phe Leu Gln Asp Ile Lys Lys Pro Asp Cys	
80 85 90	
gat gac tgg gag agc ggg ctg aat gca atg gag tgt gca tta cat ttg	398
Asp Asp Trp Glu Ser Gly Leu Asn Ala Met Glu Cys Ala Leu His Leu	
95 100 105	
gaa aaa aat gtg aat cag tca cta ctg gaa ctg cac aaa ctg gcc act	446
Glu Lys Asn Val Asn Gln Ser Leu Leu Glu Leu His Lys Leu Ala Thr	
110 115 120	
gac aaa aat gac ccc cat ttg tgt gac ttc att gag aca cat tac ctg	494
Asp Lys Asn Asp Pro His Leu Cys Asp Phe Ile Glu Thr His Tyr Leu	
125 130 135	
aat gag cag gtg aaa gcc atc aaa gaa ttg ggt gac cac gtg acc aac	542

PH-1064PCT-US seq.TXT

Asn Glu Gln Val Lys Ala Ile Lys Glu Leu Gly Asp His Val Thr Asn
140 145 150 155
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Leu Arg Lys Met Gly Ala Pro Glu Ser Gly Leu Ala Glu Tyr Leu Phe
160 165 170
gac aag cac acc ctg gga gac agt gat aat gaa agc taagcctcgg 636
Asp Lys His Thr Leu Gly Asp Ser Asp Asn Glu Ser
175 180
gctaatttcc ccatagccgt ggggtgactt ccctggtcac caaggcagtg catgcatggt 696
ggggtttcct ttaccttttc tataagttgt accaaaacat ccacttaagt tctttgattt 756
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<210> 108

<211> 183

<212> PRT

<213> Homo sapiens

<400> 108

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20 25 30
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35 40 45
Leu Lys Asn Phe Ala Lys Tyr Phe Leu His Gln Ser His Glu Glu Arg

60

PH-1064PCT-US seq.TXT

<400> 109

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 gggctgggct gtgcgcctgc gcagtgtggg tcgctcccga ttccctgccc cggccggccc 180
 cgctcgggct ccgcaccctc gccccgctct cagccgcgcg tctgccccgc agcagccagc 240
 cccgtgtccg gcagt atg ttc agc tgg gtc agc aag gat gcc cgc cgc aag 291

Met Phe Ser Trp Val Ser Lys Asp Ala Arg Arg Lys

1 5 10

aag gag ccg gag ctc ttc cag acg gtg gcc gag ggg ctg cgg cag ctg 339
 Lys Glu Pro Glu Leu Phe Gln Thr Val Ala Glu Gly Leu Arg Gln Leu

15 20 25

tac gcg cag aag ctg cta ccc ctg gag gag cac tac cgc ttc cac gag 387
 Tyr Ala Gln Lys Leu Leu Pro Leu Glu Glu His Tyr Arg Phe His Glu

30 35 40

ttc cac tcg ccc gcr ctg gag gac gct gac ttc gac aac aag cct atg 435
 Phe His Ser Pro Xaa Leu Glu Asp Ala Asp Phe Asp Asn Lys Pro Met

45 50 55 60

gtg ctc ctc gtg rgg cag tac agc acg ggc aag acc acc ttc atc cga 483
 Val Leu Leu Val Xaa Gln Tyr Ser Thr Gly Lys Thr Thr Phe Ile Arg

65 70 75

cac ctg atc gag cag gac ttc ccg ggg atg cgc atc ggg ccc gag ccc 531
 His Leu Ile Glu Gln Asp Phe Pro Gly Met Arg Ile Gly Pro Glu Pro

80 85 90

acc acc gac tcc ttc atc gcc gtc atg cac ggc ccc act gag ggc gtg 579

PH-1064PCT-US seq.TXT

Thr	Thr	Asp	Ser	Phe	Ile	Ala	Val	Met	His	Gly	Pro	Thr	Glu	Gly	Val	
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Val	Pro	Gly	Asn	Ala	Leu	Val	Val	Asp	Pro	Arg	Arg	Pro	Phe	Arg	Lys	
		110					115					120				
ctc	aac	gcg	ttt	ggc	aac	gct	ttc	ctc	aac	agg	ttc	atg	tgt	gcc	cag	675
Leu	Asn	Ala	Phe	Gly	Asn	Ala	Phe	Leu	Asn	Arg	Phe	Met	Cys	Ala	Gln	
125						130					135				140	
ctg	ccc	aac	ccc	gtc	ctg	gac	agc	atc	agc	atc	atc	gac	acc	ccc	ggg	723
Leu	Pro	Asn	Pro	Val	Leu	Asp	Ser	Ile	Ser	Ile	Ile	Asp	Thr	Pro	Gly	
				145					150					155		
atc	ctg	tct	gga	gag	aag	cag	cgg	atc	agc	aga	ggc	tat	gac	ttt	gca	771
Ile	Leu	Ser	Gly	Glu	Lys	Gln	Arg	Ile	Ser	Arg	Gly	Tyr	Asp	Phe	Ala	
		160						165					170			
gcc	gtc	ctg	gag	tgg	ttc	gcg	gag	cgt	gtg	gac	cgc	atc	atc	ctg	ctc	819
Ala	Val	Leu	Glu	Trp	Phe	Ala	Glu	Arg	Val	Asp	Arg	Ile	Ile	Leu	Leu	
		175					180						185			
ttc	gac	gcc	cac	aag	ctg	gac	atc	tcc	gat	gag	ttc	tcg	gaa	gtg	atc	867
Phe	Asp	Ala	His	Lys	Leu	Asp	Ile	Ser	Asp	Glu	Phe	Ser	Glu	Val	Ile	
		190					195					200				
aag	gct	ctg	aag	aac	cat	gag	gac	aag	atc	cgc	gtg	gtg	ctg	aac	aag	915
Lys	Ala	Leu	Lys	Asn	His	Glu	Asp	Lys	Ile	Arg	Val	Val	Leu	Asn	Lys	
205						210				215				220		
gca	gac	cag	atc	gag	acg	cag	cag	ctg	atg	cgg	gtg	tac	ggg	gcc	ctc	963

PH-1064PCT-US seq.TXT

Ala Asp Gln Ile Glu Thr Gln Gln Leu Met Arg Val Tyr Gly Ala Leu	
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235	
atg tgg tcc ctg ggc aag atc atc aac acc ccc gag gtg gtc agg gtc	1011
Met Trp Ser Leu Gly Lys Ile Ile Asn Thr Pro Glu Val Val Arg Val	
240	245
250	
tac atc ggc tcc ttc tgg tcc cac ccg ctc ctc atc ccc gac aac cgc	1059
Tyr Ile Gly Ser Phe Trp Ser His Pro Leu Leu Ile Pro Asp Asn Arg	
255	260
265	
aag ctc ttt gag gcc gag gag cag gac ctc ttc aag gac atc cag tca	1107
Lys Leu Phe Glu Ala Glu Glu Gln Asp Leu Phe Lys Asp Ile Gln Ser	
270	275
280	
ctg ccc cga aac gcc gcc ctc agg aag ctc aat gac ctg atc aag cgg	1155
Leu Pro Arg Asn Ala Ala Leu Arg Lys Leu Asn Asp Leu Ile Lys Arg	
285	290
295	300
gca cgg ctg gcc aag gtt cac gcc tac atc atc agc tcc ctc aag aaa	1203
Ala Arg Leu Ala Lys Val His Ala Tyr Ile Ile Ser Ser Leu Lys Lys	
305	310
315	
gag atg ccc aat gtc ttt ggt aaa gag agc aaa aag aaa gag ctg gtg	1251
Glu Met Pro Asn Val Phe Gly Lys Glu Ser Lys Lys Lys Glu Leu Val	
320	325
330	
aac aac ctg gga gag atc tac cag aag att gag cgc gag cac cag atc	1299
Asn Asn Leu Gly Glu Ile Tyr Gln Lys Ile Glu Arg Glu His Gln Ile	
335	340
345	
tcc cct ggg gac ttc ccg agc ctc cgc aag atg cag gaa ctc ctg cag	1347

PH-1064PCT-US seq.TXT

Ser	Pro	Gly	Asp	Phe	Pro	Ser	Leu	Arg	Lys	Met	Gln	Glu	Leu	Leu	Gln		
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Thr	Gln	Asp	Phe	Ser	Lys	Phe	Gln	Ala	Leu	Lys	Pro	Lys	Leu	Leu	Asp		
365					370					375					380		
acg	gtg	gat	gac	atg	ctg	gcc	aac	gac	atc	gcg	cgg	ctg	atg	gtg	atg	1443	
Thr	Val	Asp	Asp	Met	Leu	Ala	Asn	Asp	Ile	Ala	Arg	Leu	Met	Val	Met		
				385					390					395			
gtg	cgg	cag	gag	gag	tcc	ctg	atg	cct	tcc	cag	gtg	gtc	aag	ggc	ggc	1491	
Val	Arg	Gln	Glu	Glu	Ser	Leu	Met	Pro	Ser	Gln	Val	Val	Lys	Gly	Gly		
			400					405					410				
gcc	ttt	gac	ggc	acc	atg	aac	ggg	ccg	ttc	ggg	cac	ggc	tac	ggc	gag	1539	
Ala	Phe	Asp	Gly	Thr	Met	Asn	Gly	Pro	Phe	Gly	His	Gly	Tyr	Gly	Glu		
			415					420					425				
ggg	gcc	ggc	gag	ggc	atc	cac	gac	gtg	gag	tgg	gtg	gtg	ggc	aag	gac	1587	
Gly	Ala	Gly	Glu	Gly	Ile	His	Asp	Val	Glu	Trp	Val	Val	Gly	Lys	Asp		
			430					435					440				
aag	ccc	acc	tac	gac	gag	atc	ttc	tac	acg	ctg	tcc	cct	gtc	aac	ggc	1635	
Lys	Pro	Thr	Tyr	Asp	Glu	Ile	Phe	Tyr	Thr	Leu	Ser	Pro	Val	Asn	Gly		
445					450					455				460			
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Lys	Ile	Thr	Gly	Ala	Asn	Ala	Lys	Lys	Glu	Met	Val	Lys	Ser	Lys	Leu		
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ccc	aac	acc	gtg	cta	ggg	aag	atc	tgg	aag	ctg	gcc	gac	gtg	gac	aag	1731	

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Pro Asn Thr Val Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys
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Asp Gly Leu Leu Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile
495 500 505
aag gtc aag ctg gag ggc cac gag ctg ccc gcc gac ctg ccc ccg cac 1827
Lys Val Lys Leu Glu Gly His Glu Leu Pro Ala Asp Leu Pro Pro His
510 515 520
ctg gtg ccg ccc tcc aag cgc aga cat gag tgatggcgcc cggccccgca 1877
Leu Val Pro Pro Ser Lys Arg Arg His Glu
525 530
cctgccattt gcacgcccgg ccgggaggca gagacggggg gaggggaagc ctcaccattt 1937
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<210> 110

<211> 534

<212> PRT

<213> Homo sapiens

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<221> unsure

<222> (49)

<223>

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PH-1064PCT-US seq.TXT

<221> unsure

<222> (65)

<223>

<400> 110

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				20					25					30	
Leu	Leu	Pro	Leu	Glu	Glu	His	Tyr	Arg	Phe	His	Glu	Phe	His	Ser	Pro
				35					40					45	
Xaa	Leu	Glu	Asp	Ala	Asp	Phe	Asp	Asn	Lys	Pro	Met	Val	Leu	Leu	Val
				50					55					60	
Xaa	Gln	Tyr	Ser	Thr	Gly	Lys	Thr	Thr	Phe	Ile	Arg	His	Leu	Ile	Glu
				65					70					75	
Gln	Asp	Phe	Pro	Gly	Met	Arg	Ile	Gly	Pro	Glu	Pro	Thr	Thr	Asp	Ser
				85					90					95	
Phe	Ile	Ala	Val	Met	His	Gly	Pro	Thr	Glu	Gly	Val	Val	Pro	Gly	Asn
				100					105					110	
Ala	Leu	Val	Val	Asp	Pro	Arg	Arg	Pro	Phe	Arg	Lys	Leu	Asn	Ala	Phe
				115					120					125	
Gly	Asn	Ala	Phe	Leu	Asn	Arg	Phe	Met	Cys	Ala	Gln	Leu	Pro	Asn	Pro
				130					135					140	
Val	Leu	Asp	Ser	Ile	Ser	Ile	Ile	Asp	Thr	Pro	Gly	Ile	Leu	Ser	Gly
				145					150					155	
															160

PH-1064PCT-US seq.TXT

Glu	Lys	Gln	Arg	Ile	Ser	Arg	Gly	Tyr	Asp	Phe	Ala	Ala	Val	Leu	Glu
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Trp	Phe	Ala	Glu	Arg	Val	Asp	Arg	Ile	Ile	Leu	Leu	Phe	Asp	Ala	His
			180					185					190		
Lys	Leu	Asp	Ile	Ser	Asp	Glu	Phe	Ser	Glu	Val	Ile	Lys	Ala	Leu	Lys
		195					200						205		
Asn	His	Glu	Asp	Lys	Ile	Arg	Val	Val	Leu	Asn	Lys	Ala	Asp	Gln	Ile
	210					215					220				
Glu	Thr	Gln	Gln	Leu	Met	Arg	Val	Tyr	Gly	Ala	Leu	Met	Trp	Ser	Leu
225					230				235					240	
Gly	Lys	Ile	Ile	Asn	Thr	Pro	Glu	Val	Val	Arg	Val	Tyr	Ile	Gly	Ser
			245					250					255		
Phe	Trp	Ser	His	Pro	Leu	Leu	Ile	Pro	Asp	Asn	Arg	Lys	Leu	Phe	Glu
		260						265					270		
Ala	Glu	Glu	Gln	Asp	Leu	Phe	Lys	Asp	Ile	Gln	Ser	Leu	Pro	Arg	Asn
		275					280						285		
Ala	Ala	Leu	Arg	Lys	Leu	Asn	Asp	Leu	Ile	Lys	Arg	Ala	Arg	Leu	Ala
	290					295					300				
Lys	Val	His	Ala	Tyr	Ile	Ile	Ser	Ser	Leu	Lys	Lys	Glu	Met	Pro	Asn
305					310					315				320	
Val	Phe	Gly	Lys	Glu	Ser	Lys	Lys	Lys	Glu	Leu	Val	Asn	Asn	Leu	Gly
			325						330				335		
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Phe Pro Ser Leu Arg Lys Met Gln Glu Leu Leu Gln Thr Gln Asp Phe
355 360 365

Ser Lys Phe Gln Ala Leu Lys Pro Lys Leu Leu Asp Thr Val Asp Asp
370 375 380

Met Leu Ala Asn Asp Ile Ala Arg Leu Met Val Met Val Arg Gln Glu
385 390 395 400

Glu Ser Leu Met Pro Ser Gln Val Val Lys Gly Gly Ala Phe Asp Gly
405 410 415

Thr Met Asn Gly Pro Phe Gly His Gly Tyr Gly Glu Gly Ala Gly Glu
420 425 430

Gly Ile His Asp Val Glu Trp Val Val Gly Lys Asp Lys Pro Thr Tyr
435 440 445

Asp Glu Ile Phe Tyr Thr Leu Ser Pro Val Asn Gly Lys Ile Thr Gly
450 455 460

Ala Asn Ala Lys Lys Glu Met Val Lys Ser Lys Leu Pro Asn Thr Val
465 470 475 480

Leu Gly Lys Ile Trp Lys Leu Ala Asp Val Asp Lys Asp Gly Leu Leu
485 490 495

Asp Asp Glu Glu Phe Ala Leu Ala Asn His Leu Ile Lys Val Lys Leu
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Met Gly Glu Ile Lys Val Ser Pro

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gat tat aac tgg ttt aga ggt aca gtt ccc ctt aaa aag att att gtg 160
Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val

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gat gat gat gac agt aag ata tgg tcg ctc tat gac gcg ggc ccc cga 208
Asp Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg

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35

40

agt atc agg tgt cct ctc ata ttc ctg ccc cct gtc agt gga act gca 256
Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala

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gat gtc ttt ttc cgg cag att ttg gct ctg act gga tgg ggt tac cgg 304
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65

70

PH-1064PCT-US seq.TXT

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gat gga ttc aga aaa ctt tta gac cat tta caa ttg gat aaa gtt cat      400
Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His
      90                      95                      100

ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc cag aaa ttt gct gaa      448
Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu
105                      110                      115                      120

tac act cac aaa tct cct aga gtc cat tcc cta atc ctc tgc aat tcc      496
Tyr Thr His Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser
      125                      130                      135

ttc agt gac acc tct atc ttc aac caa act tgg act gca aac agc ttt      544
Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe
      140                      145                      150

tgg ctg atg cct gca ttt atg ctc aaa aaa ata gtt ctt gga aat ttt      592
Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe
      155                      160                      165

tca tct ggc ccg gtg gac cct atg atg gct gat gcc att gat ttc atg      640
Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met
      170                      175                      180

gta gac agg cta gaa agt ttg ggt cag agt gaa ctg gct tca aga ctt      688
Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu
185                      190                      195                      200

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Thr Leu Lys Leu Ser Lys Phe Leu Cys Gly Thr Ser

                205                210

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<212> PRT

<213> Homo sapiens

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Val	Pro	Leu	Lys	Lys	Ile	Ile	Val	Asp	Asp	Asp	Asp	Ser	Lys	Ile	Trp
				20					25					30	
Ser	Leu	Tyr	Asp	Ala	Gly	Pro	Arg	Ser	Ile	Arg	Cys	Pro	Leu	Ile	Phe
				35					40					45	
Leu	Pro	Pro	Val	Ser	Gly	Thr	Ala	Asp	Val	Phe	Phe	Arg	Gln	Ile	Leu
				50					55					60	
Ala	Leu	Thr	Gly	Trp	Gly	Tyr	Arg	Val	Ile	Ala	Leu	Gln	Tyr	Pro	Val
				65					70					75	
Tyr	Trp	Asp	His	Leu	Glu	Phe	Cys	Asp	Gly	Phe	Arg	Lys	Leu	Leu	Asp
				85					90					95	
His	Leu	Gln	Leu	Asp	Lys	Val	His	Leu	Phe	Gly	Ala	Ser	Leu	Gly	Gly
				100					105					110	
Phe	Leu	Ala	Gln	Lys	Phe	Ala	Glu	Tyr	Thr	His	Lys	Ser	Pro	Arg	Val
				115					120					125	
His	Ser	Leu	Ile	Leu	Cys	Asn	Ser	Phe	Ser	Asp	Thr	Ser	Ile	Phe	Asn
				130					135					140	
Gln	Thr	Trp	Thr	Ala	Asn	Ser	Phe	Trp	Leu	Met	Pro	Ala	Phe	Met	Leu
				145					150					155	
Lys	Lys	Ile	Val	Leu	Gly	Asn	Phe	Ser	Ser	Gly	Pro	Val	Asp	Pro	Met
				165					170					175	
Met	Ala	Asp	Ala	Ile	Asp	Phe	Met	Val	Asp	Arg	Leu	Glu	Ser	Leu	Gly
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PH-1064PCT-US seq.TXT

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205

Cys Gly Thr Ser

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10

15

kcw tty kkc tcc aaa acg tgg att gag gtc tca ggt tcc tct scc aaa 96

Xaa Xaa Xaa Ser Lys Thr Trp Ile Glu Val Ser Gly Ser Ser Xaa Lys

20

25

30

gat gyt kca aag cag ctg aag gag cag cag atg gtg atg aga ggc cac 144

Asp Xaa Xaa Lys Gln Leu Lys Glu Gln Gln Met Val Met Arg Gly His

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gcg gcc ttt ggt ggg ctg tgc atc ggg gcc ctc tcg gtc ctg gct gac	240		
Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp			
65	70	75	80
ttc cta ggc gcc att ggg tct gga acc ggg atc ctg ctc gca gtc aca	288		
Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr			
85	90	95	
atc atc tac cag tac ttt gag atc ttc gtt aag gag yaa agc gag gtt	336		
Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val			
100	105	110	
ggc agc atg ggg gcc ctg ctc ttc tgagcccgtc tcccggacag gttgaggaag	390		
Gly Ser Met Gly Ala Leu Leu Phe			
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 35 40 45

Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr Ile Pro Thr Ala
 50 55 60

Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser Val Leu Ala Asp
 65 70 75 80

Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu Leu Ala Val Thr
 85 90 95

Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu Xaa Ser Glu Val
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Gly Ser Met Gly Ala Leu Leu Phe
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20

cacagttcca gganngggta ggtagcagtg tgtgtgttat gtgccactga ccctgaaara 1
80

tgtgccatag cccaagccaa ttgaaattga tcagggggcc aggcacggtg gctcatgcct 2
40

gtaatcccag caccttggga agctgaggtg ggaggattgc ttgaaaccag gagttcaaga 3
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Ser Trp Ala Asn Leu Ser Arg Thr Cys Phe Pro Glu Ala Arg Cys Ser

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15

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25

gtg acc cag cgc atc tta acc ttg ggt ctc cta ggc tcg agg cta ggg 148

Val Thr Gln Arg Ile Leu Thr Leu Gly Leu Leu Gly Ser Arg Leu Gly

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cat tac gtt tcg tgg aac caa agc agc caa ttg cat agc aag tat ttt 196

His Tyr Val Ser Trp Asn Gln Ser Ser Gln Leu His Ser Lys Tyr Phe

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cct gca ttc caa tta aat gct taagaaaaag cagcatccta taaaattgtg 247

PH-1064PCT-US seq.TXT
Pro Ala Phe Gln Leu Asn Ala

60

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20

25

30

Leu Gly Leu Leu Gly Ser Arg Leu Gly His Tyr Val Ser Trp Asn Gln

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40

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Ser Ser Gln Leu His Ser Lys Tyr Phe Pro Ala Phe Gln Leu Asn Ala

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aagcccctcg aattctgtga aaatgagggt ttcttaactc aactgagag cggaaggagg 240
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PH-1064PCT-US seq.TXT

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 aagcaatagc agcaggagtc cccagcagct ggagccgcaa gaatgaactg caaagaggga 480
 actgacagca gctgcggctg cagggggcaa cgacgagaag aag atg ttg aag tgt 535

Met Leu Lys Cys

1

gtg gtg gtg ggg gac ggt gcc gtg ggg aaa acc tgc ctg ctg atg agc 583
 Val Val Val Gly Asp Gly Ala Val Gly Lys Thr Cys Leu Leu Met Ser
 5 10 15 20

tac gcc aac gac gcc ttc cca gag gaa tac gtg ccc act gtg ttt gac 631
 Tyr Ala Asn Asp Ala Phe Pro Glu Glu Tyr Val Pro Thr Val Phe Asp
 25 30 35

cac tat gca gtt act gtg act gtg gga ggc aag caa cac ttg ctc gga 679
 His Tyr Ala Val Thr Val Thr Val Gly Gly Lys Gln His Leu Leu Gly
 40 45 50

ctg tat gac acc gcg gga cag gag gac tac aac cag ctg agg cca ctc 727
 Leu Tyr Asp Thr Ala Gly Gln Glu Asp Tyr Asn Gln Leu Arg Pro Leu
 55 60 65

tcc tac ccc aac acg gat gtg ttt ttg atc tgc ttc tct gtc gta aac 775
 Ser Tyr Pro Asn Thr Asp Val Phe Leu Ile Cys Phe Ser Val Val Asn
 70 75 80

cct gcc tct tac cac aat gtc cag gag gaa tgg gtc ccc gag ctc aag 823
 Pro Ala Ser Tyr His Asn Val Gln Glu Glu Trp Val Pro Glu Leu Lys
 85 90 95 100

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gac tgc atg cct cac gtg cct tat gtc ctc ata ggg acc cag att gat	871
Asp Cys Met Pro His Val Pro Tyr Val Leu Ile Gly Thr Gln Ile Asp	
105 110 115	
ctc cgt gat gac cca aaa acc ttg gcc cgt ttg ctg tat atg aaa gag	919
Leu Arg Asp Asp Pro Lys Thr Leu Ala Arg Leu Leu Tyr Met Lys Glu	
120 125 130	
aaa cct ctc act tac gag cat ggt gtg aag ctc gca aaa gcg atc gga	967
Lys Pro Leu Thr Tyr Glu His Gly Val Lys Leu Ala Lys Ala Ile Gly	
135 140 145	
gca cag tgc tac ttg gaa tgt tca gct ctg act cag aaa ggt ctc aaa	1015
Ala Gln Cys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Lys Gly Leu Lys	
150 155 160	
gcg gtt ttt gat gaa gca atc ctc acc att ttc cac ccc aag aaa aag	1063
Ala Val Phe Asp Glu Ala Ile Leu Thr Ile Phe His Pro Lys Lys Lys	
165 170 175 180	
aag aaa cgc tgt tct gag ggt cac agc tgc tgt tca att atc	1105
Lys Lys Arg Cys Ser Glu Gly His Ser Cys Cys Ser Ile Ile	
185 190	
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<210> 120

<211> 194

<212> PRT

<213> Homo sapiens

<400> 120

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Leu	Leu	Met	Ser	Tyr	Ala	Asn	Asp	Ala	Phe	Pro	Glu	Glu	Tyr	Val	Pro
				20				25					30		
Thr	Val	Phe	Asp	His	Tyr	Ala	Val	Thr	Val	Thr	Val	Gly	Gly	Lys	Gln
				35				40					45		
His	Leu	Leu	Gly	Leu	Tyr	Asp	Thr	Ala	Gly	Gln	Glu	Asp	Tyr	Asn	Gln
				50				55					60		
Leu	Arg	Pro	Leu	Ser	Tyr	Pro	Asn	Thr	Asp	Val	Phe	Leu	Ile	Cys	Phe
65					70					75				80	
Ser	Val	Val	Asn	Pro	Ala	Ser	Tyr	His	Asn	Val	Gln	Glu	Glu	Trp	Val
				85					90					95	
Pro	Glu	Leu	Lys	Asp	Cys	Met	Pro	His	Val	Pro	Tyr	Val	Leu	Ile	Gly
				100					105					110	
Thr	Gln	Ile	Asp	Leu	Arg	Asp	Asp	Pro	Lys	Thr	Leu	Ala	Arg	Leu	Leu
				115					120					125	
Tyr	Met	Lys	Glu	Lys	Pro	Leu	Thr	Tyr	Glu	His	Gly	Val	Lys	Leu	Ala
				130					135					140	
Lys	Ala	Ile	Gly	Ala	Gln	Cys	Tyr	Leu	Glu	Cys	Ser	Ala	Leu	Thr	Gln
145					150					155				160	
Lys	Gly	Leu	Lys	Ala	Val	Phe	Asp	Glu	Ala	Ile	Leu	Thr	Ile	Phe	His
				165					170					175	
Pro	Lys	Lys	Lys	Lys	Lys	Arg	Cys	Ser	Glu	Gly	His	Ser	Cys	Cys	Ser
				180						185				190	

Ile Ile

<210> 121

<211> 1732

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (2)..(259)

<220>

<221> unsure

<222> (28)

<223> a,c,g or t

<220>

<221> unsure

<222> (388)

<223> g or a

<220>

<221> unsure

<222> (631)

<223> a or t

<220>

<221> unsure

<222> (637)

PH-1064PCT-US seq.TXT

<223> g or a

<220>

<221> unsure

<222> (638)

<223> g or a

<220>

<221> unsure

<222> (639)

<223> g or a

<400> 121

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Asp Ile Glu Ser Lys Glu Gln Val Xaa Thr Leu Thr Gly His Val Gly

1

5

10

15

acc gtg tat gcc ctg gcg gtc atc tcg acg cca gac cag acc aaa gtc 97

Thr Val Tyr Ala Leu Ala Val Ile Ser Thr Pro Asp Gln Thr Lys Val

20

25

30

ttc agt gca tcc tac gac cgg tcc ctc agg gtc tgg agt atg gac aac 145

Phe Ser Ala Ser Tyr Asp Arg Ser Leu Arg Val Trp Ser Met Asp Asn

35

40

45

atg atc tgc acg cag acc ctg ctg cgt cac cag ggc agt gtc acc gcg 193

Met Ile Cys Thr Gln Thr Leu Leu Arg His Gln Gly Ser Val Thr Ala

50

55

60

ctg gct gtg tcc cgg ggc cga ctc ttc tca ggg gct gtg gat agc act 241

Leu Ala Val Ser Arg Gly Arg Leu Phe Ser Gly Ala Val Asp Ser Thr

65

70

75

80

gtg aag gtt tgg act tgc taacaggatc caggccaggc tgtggtttcc

289

Val Lys Val Trp Thr Cys

85

cctgaaccag ccctggacct ttctgagcca ggctggccac atgggggtggt ctgggggttt 349
 ctgcctgccc cgtgggcata ggtggacagg ctctggcarg ccggcagtgcc cctccccgtc 409
 ccatgctcgg cgagcctccc tctactcggc actgtccttg ctgcccagcc cctctctggg 469
 tgccaggtag gacgcttgcc ccggcccacc ctccatcccc accctccatc cccaccctag 529
 atggagcgag ggccttttta ctacactttt ctaccgtttt tagactgtat gtagatttgg 589
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 gggacaaggg ggctgtgtgt ggccttgagg ttggtgtgca caggcactgg ctgctgtgag 709
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 cgccccacac cacaatcgct ggttttcggc attttttaaa tttttttttt aagaaacgtc 1129
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 tacatgccct gcttccacgt ggctgccacg ctgacacacc cacattcacc aaaccacccc 1429
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PH-1064PCT-US seq.TXT

tcgagttctt ggggcgcaga gaacttagga gagaagcacg gaggagcccc cggcagagca 1549
 cccgcccccg ggccccagcc ttccacctgt gctagcagcc tggggcctcc actctggccg 1609
 gaggaaggac cgcaggcaga cagcctgggc ctctaacagc ttttgtccgg agctagactt 1669
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<210> 122

<211> 86

<212> PRT

<213> Homo sapiens

<220>

<221> unsure

<222> (9)

<223> unknown

<400> 122

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1				5					10					15	
Thr	Val	Tyr	Ala	Leu	Ala	Val	Ile	Ser	Thr	Pro	Asp	Gln	Thr	Lys	Val
				20					25					30	
Phe	Ser	Ala	Ser	Tyr	Asp	Arg	Ser	Leu	Arg	Val	Trp	Ser	Met	Asp	Asn
				35				40						45	
Met	Ile	Cys	Thr	Gln	Thr	Leu	Leu	Arg	His	Gln	Gly	Ser	Val	Thr	Ala
				50				55						60	
Leu	Ala	Val	Ser	Arg	Gly	Arg	Leu	Phe	Ser	Gly	Ala	Val	Asp	Ser	Thr
65						70								75	80

PH-1064PCT-US seq.TXT

Val Lys Val Trp Thr Cys

85

<210> 123

<211> 603

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (168)..(350)

<220>

<221> unsure

<222> (343)

<223> g or a

<220>

<221> unsure

<222> (422)

<223> t or c

<220>

<221> unsure

<222> (457)

<223> g or c

<400> 123

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gccaaacttg gttgaagact aggtcttccc tggcaagttc cggaaga atg gac tta 176

Met Asp Leu

1

ctg act ttt atc aac tct tct cac tgc caa ggc caa cag cat ctg agg 224

Leu Thr Phe Ile Asn Ser Ser His Cys Gln Gly Gln Gln His Leu Arg

5

10

15

tat agc ttt ttg gga gta cct gct ttc ttg cct cct gga gga tat ttt 272

Tyr Ser Phe Leu Gly Val Pro Ala Phe Leu Pro Pro Gly Gly Tyr Phe

20

25

30

35

ctg tcc tgg ggc ttc atg gcc cct ctc ttc cct gtt aca cat tgc tgt 320

Leu Ser Trp Gly Phe Met Ala Pro Leu Phe Pro Val Thr His Cys Cys

40

45

50

gct tca gag cct ttg cag ctg cra cct agt tgaatccaca taggsttcct 370

Ala Ser Glu Pro Leu Gln Leu Xaa Pro Ser

55

60

tccacacggt ggggaaggatc ttgctgcttt cactcacagg accagggagt tyttcaatca 430

ggaggtgggt ttttgttccc ttcaggsctt tggcaacatc tagagacagt tttgattgcc 490

acgcctggag tgggatgtgt gtgctactgg catctagtgg ctgctaaaca tcctacactg 550

cataggatag tccccactac ccccagccaa gaattatctg actccagggg tca 603

<210> 124

<211> 61

<212> PRT

<213> Homo sapiens

PH-1064PCT-US seq.TXT

<220>

<221> unsure

<222> (59)

<223> unknown

<400> 124

Met	Asp	Leu	Leu	Thr	Phe	Ile	Asn	Ser	Ser	His	Cys	Gln	Gly	Gln	Gln
1				5					10					15	
His	Leu	Arg	Tyr	Ser	Phe	Leu	Gly	Val	Pro	Ala	Phe	Leu	Pro	Pro	Gly
				20				25						30	
Gly	Tyr	Phe	Leu	Ser	Trp	Gly	Phe	Met	Ala	Pro	Leu	Phe	Pro	Val	Thr
			35					40						45	
His	Cys	Cys	Ala	Ser	Glu	Pro	Leu	Gln	Leu	Xaa	Pro	Ser			
			50					55				60			

<210> 125

<211> 1289

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (775)..(1017)

<220>

<221> unsure

<222> (200)

PH-1064PCT-US seq.TXT

<223> g or a

<400> 125

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ttttccctga ctccagcagg gcaaggaatg taaccgagag gttgtgtggg ctgggctctg 180
gtgccctctt cctgggccc gaacacctct cctcctgatt cccttggcac cttgtctttc 240
tgtctgttta cctgtctccc tgcctgcca tctgcatctt ttgcagccca ctctgacttc 300
catctggggg ctgagaccac ccttgccctgc ccccttcttt ctgccttaag aatgtccttt 360
taggctgggc atggttgta cgctgtaac ccagcactt tgggaggcgg agacgggcag 420
ataacctgag gtcaggatTT cgagaccaac ctgacctaca tggagaaact ccgcctctag 480
taaaaataca aaattagccg ggcattgttg tgcacgcctc taatcccagc tactcgggag 540
gctgaggcag gagaatcact tgaacccggg aagtggaggt tgcagtgagc caagagtaca 600
ccactgcact ccagcctggg caacagagcg agactccgtc ttaaaaaaaaa aaaaaaaaaag 660
aacgcccttt tactgtcctc atcatcccag tttgaggcag tgctggagtg gggaaggccg 720
tcttagacca tagaggttgg aagacgctga gagatcatcc agcccagccc cttg atg 777

Met

1

tta cag agc aga aga cag atg ccc aaa cag gag aag gca ctt gcc cac 825
Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala His
5 10 15
ggc cat acg gca ggc tgc cac aaa acc aag atg gca gcc ctt cct cag 873
Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro Gln
20 25 30
cgt gcc tca ctg cca ctc cca gag cca ggg agc ccc ata aaa ccc aca 921

PH-1064PCT-US seq.TXT

Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro Thr
 35 40 45
 tca tgt ctt aag agt ata tct ggc tcc ttg acc agc aat cgg ccc tgg 969
 Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro Trp
 50 55 60 65
 gag cca cca ggt ggg aaa agc gcc tct gcc aga gtc cag gcc ttg gga 1017
 Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu Gly
 70 75 80
 tgacagacag cttgcccgca cactcggggc ccactcaagg atgtaggggc ttttctggcc 1077
 cctgaccctt ccctgggcat tgggagcgtg gggacggggc tggccttggg aggagcggca 1137
 ggggcatcac ctctttctgc tgcttctccc tgctcctacc ctcaagggcc tgggggctgc 1197
 ccagctgcct ctatgccctt ctgggggtct cagcccactg ctgacacttc tgcaatccag 1257
 agaaacacta aataaagcaa tacgtgtttg cc 1289

<210> 126

<211> 81

<212> PRT

<213> Homo sapiens

<400> 126

Met Leu Gln Ser Arg Arg Gln Met Pro Lys Gln Glu Lys Ala Leu Ala
 1 5 10 15
 His Gly His Thr Ala Gly Cys His Lys Thr Lys Met Ala Ala Leu Pro
 20 25 30
 Gln Arg Ala Ser Leu Pro Leu Pro Glu Pro Gly Ser Pro Ile Lys Pro
 35 40 45

PH-1064PCT-US seq.TXT

Thr Ser Cys Leu Lys Ser Ile Ser Gly Ser Leu Thr Ser Asn Arg Pro
 50 55 60
 Trp Glu Pro Pro Gly Gly Lys Ser Ala Ser Ala Arg Val Gln Ala Leu
 65 70 75 80
 Gly

<210> 127

<211> 1085

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (734)..(886)

<220>

<221> unsure

<222> (276)

<223> g or t

<400> 127

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 ggaattacag gcacgcacca ccatgcctga ctaattttgt attttttagta gacatgggggt 180
 ttctccatgt tggtcaggct ggtctcaaac tcccaccttc aggtgatccg cccacctcgg 240
 cctcctgagg tggctgagat tacaggcgtg caactkgtgc cagcttgcta attttcacag 300

PH-1064PCT-US seq.TXT

aagttgatgg caattcttca catgtaaaca gtgccagtgc acagaacctt tatatatattt 360
 ttgaagccag tactgtgctc tgcatataac aaagctgctt caaggatgag acctttttct 420
 aaaagcatgt aatgtgagaa gccggcctgc cttatatttct tttttctttt ttaatgatta 480
 aaaatagttt gtggcaaggc acggtggctc aggcctgtaa ttctagcact ttgggaggcc 540
 gaggcaggag gattacttga gcctacaagt ttgatgggcc agcatgcaca gcatagcaag 600
 actgcatctc tacagagagt aaaaaaaatt acccgagtgt ggtgatgtgc atctgtaatc 660
 tcagctactt gggaggctga ggtgagagga tcacttgagc ttgggtgagg tgaggctgca 720
 gtgagtcctg atc atg ctg ctg cac tca atc ttg gac aac aga gca aga 769

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg

1 5 10

ccc tgt ctc aaa aaa aaa aaa aat ata tat ata tat ata tat tat ttt 817

Pro Cys Leu Lys Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe

15 20 25

tat gag gtg aag tgc atc aaa ctt ggg aaa gat ttg agg agg ctg gga 865

Tyr Glu Val Lys Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly

30 35 40

acc tcc tgg aaa acc act cct tgaagaaaga tatgagagac atttagaagt 916

Thr Ser Trp Lys Thr Thr Pro

45 50

gattcctgct ttcagaagga ggtggattca aatacatcaa aagtccttc ctctgctaag 976

tgtttatagt tcaatgaata atttcaatat ttgtatgtgt tcttgtcatt ttattttttt 1036

ctgaaaaact tccaaaaatt tgaaaataaa attacagcct tttcttctt 1085

<210> 128

<211> 51

PH-1064PCT-US seq.TXT

<212> PRT

<213> Homo sapiens

<400> 128

Met Leu Leu His Ser Ile Leu Asp Asn Arg Ala Arg Pro Cys Leu Lys

1

5

10

15

Lys Lys Lys Asn Ile Tyr Ile Tyr Ile Tyr Tyr Phe Tyr Glu Val Lys

20

25

30

Cys Ile Lys Leu Gly Lys Asp Leu Arg Arg Leu Gly Thr Ser Trp Lys

35

40

45

Thr Thr Pro

50

<210> 129

<211> 1544

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (1076)

<223> g or a

<400> 129

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60

PH-1064PCT-US seq.TXT

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attaactctt gtggacagtc cctaaaagtc cagttctaca tttgtgaaaa ttgtggtgcc 40	2
atgaattaag atggatgact ggaaaaaggt gttggagaaa gagttaaaga tgaggaagag 00	3
atatttttag tatatgaagt tatccaggga cttgatattc ataattcagt gctgtggaaa 60	3
tgaaaaaaat gattgaagag gtggaacgga aatgacctta gggggaaaaa aaaggaccaa 20	4
agaagtctga ttaaaagttg aaatcagtat ttctgaattc aaattgcttg aatttcctaaa 80	4
atagtcagta aaggatctaa tagaaccaga attatttggg tgaattctgc aggttttatg 40	5
ggcttgtcac aacgtgaagg gctggaatgt atattaccaa atgggaattt ccattgtagg 00	6
tttttgctag tcccaccccc attttagcct aatttggcct aaacgcagta tggggagaat 60	6

PH-1064PCT-US seq.TXT

tgttcccatt ccatgtgttc tgaattcagc tcctctccca gcatatagat atctcctcct 7
20

ttaactccga ccagaaccct tcttctgtg gcactcccca cccatagacc ttcagatcat 7
80

ctcccacacc ctggatctca ctctcctctt agtaacagag acactcctga gggttgactt 8
40

ccttgctttt ctctacttcc aaatcacaat ttcttacaac caagctttgt gctcccgagt 9
00

aagcagggat gtactagggg aatgtaaaac tgcaaactta aaaacctgca tcttcttgaa 9
60

gcatcagttt tacttaccaa atgggtttaga gtcataagat gacctatttt tatataaaag 10
20

ttatattata gaataaaatg ttcatacgca tagactgtta agataaaaaa ataggraatc 10
80

ttgcaaggta attcttattt gcaagtgggt tatgtgttca ctctcctcta cctttatggt 11
40

attttggtgt tcacttacga agcatacaac tagaaccata tccaagcaga ctctggggtg 12
00

ctgttaaccc agggcctaga cttctagtgc ctctgaggca gaaccaaagg agcctgcact 12

60

gggggaaatc ccttttcctg cctgcctgtc tgcctgtgac ctgtgtacgt attacaggct 13
20

ttaggaccag ctgattgtta tgcttgcagg atggttttga aacagaaaca atacttgttt 13
80

actgtaggaa tcctatttat attatTTTTc agtcctgtga atgctgtgaa aagatttatt 14
40

cctttgaggc caggaagctc ccaggcatat atgcttctag gttaggattg tcctgactca 15
00

ctaaagatgc caggatattg gggctgaggg gagtttgagg tgtt 15
44

<210> 130

<211> 508

<212> DNA

<213> Homo sapiens

<400> 130

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atgggaaaca ggttatcggg ggattcatga agtcagtgag agtaattgct tcttttttgc 1
20

PH-1064PCT-US seq.TXT

gggtgaactg aatgtatttc ttcaccaa at cttgatgtta acaattaaaa agaagaaatg 1
80

acatgcaagt aggtcttagc agaaaaatgc aggctgggca tgagtcatgt tgttaccctc 2
40

ccacatgctc ctacaatcca cagagatgcc tgtctgcagg ttcttgaagt tattgttagt 3
00

atttggtatc tcaaattttt cgtcactggt cacatgccac tttctctgtg cacagtggta 3
60

tcctcatttg ctttttaacc tacactgagg agtctttgtc aggttgcact gattttccaa 4
20

ttctgcagta atgagtaagc tcacggcatg gggaagaaga cagtcagtcc aatgaagtgc 4
80

tctaaattat tttaacattg cctttgaa 5
08

<210> 131

<211> 1204

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (50)

<223> g or t

<220>

<221> unsure

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<223> g or c

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<221> unsure

<222> (300)

<223> g or c

<220>

<221> unsure

<222> (407)

<223> g or a

<220>

<221> unsure

<222> (415)

<223> a,c,g or t

<220>

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Tyr Leu Ser Pro Gln Gln Gly Ser Gln Asn His Phe Asp Pro Pro Leu

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25

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Ala Glu Gly Ser Pro Leu Tyr Arg Val Gln Ser Leu Lys Ala Trp Ile

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agc tgt taatctcatt ggaggaggga actgtttcct gcattcattc atctgggaac 201

Ser Cys

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aaaaccaagg tctttcttcc agcgaattta tctccttcag gaagctgggt cctgccacca 321

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agc tat cct ttc aaa cag cta ttg gca agt ttt aaa ccc aaa ata tat 585

Ser Tyr Pro Phe Lys Gln Leu Leu Ala Ser Phe Lys Pro Lys Ile Tyr

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aca cat agt tct gta ata aaa ctg ttt gac ttc tca agt aac atg act 633

Thr His Ser Ser Val Ile Lys Leu Phe Asp Phe Ser Ser Asn Met Thr

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tcc tta ttt ctg aac agt act ggt tac ttt caa aat gaa ttt tta ttg 681

Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu Leu

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aga ttt tcc att aac tat ttt ttt caa aga ctc aaa ttt tgt acc aag 729

Arg Phe Ser Ile Asn Tyr Phe Phe Gln Arg Leu Lys Phe Cys Thr Lys

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25

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Thr Ser Leu Phe Leu Asn Ser Thr Gly Tyr Phe Gln Asn Glu Phe Leu

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Lys

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Asn Thr Gly Cys Ile Pro Pro Ala Arg Asp Phe Tyr Leu Arg Arg Pro

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Met Lys His

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Met Ser Leu Ser

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	25	30	35	
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Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu Ala Ala Ser Ser				
	40	45	50	
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Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile Cys Ile Ser Ser				
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His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val Phe Thr Glu Ile				
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<213> Homo sapiens

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30

Thr Ile Ile Val Glu Asp Thr Lys Phe Lys Ala His Ser Asn Val Leu

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40

45

Ala Ala Ser Ser Leu Tyr Phe Lys Asn Ile Phe Trp Ser His Thr Ile

50

55

60

Cys Ile Ser Ser His Val Leu Glu Leu Asp Asp Leu Lys Ala Glu Val

65

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75

80

Phe Thr Glu Ile Leu Asn Tyr Ile Tyr Ser Ser Thr Val Val Val Lys

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Arg Gln Glu Thr Val Thr Asp Leu Ala Ala Ala Gly Lys Lys Leu Gly

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105

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Ile Ser Phe Leu Glu Asp Leu Thr Asp Arg Asn Phe Ser Asn Ser Pro

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<222> (138)..(1307)

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cccggccagg gagggcc atg att tcc ctc ccg ggg ccc ctg gtg acc aac 170
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Leu Leu Arg Phe Leu Phe Leu Gly Leu Ser Ala Leu Ala Pro Pro Ser
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Arg Ala Gln Leu Gln Leu His Leu Pro Ala Asn Arg Leu Gln Ala Val
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gag gga ggg gaa gtg gtg ctt cca gcg tgg tac acc ttg cac ggg gag 314
Glu Gly Gly Glu Val Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu
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Pro	Ser	Cys	Arg	Leu	Gln	Gly	Val	Pro	His	Val	Gly	Ala	Asn	Val	Thr		
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Leu	Ser	Cys	Gln	Ser	Pro	Arg	Ser	Lys	Pro	Ala	Val	Gln	Tyr	Gln	Trp		
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gat	cgg	cag	ctt	cca	tcc	ttc	cag	act	ttc	ttt	gca	cca	gca	tta	gat	746	

Asp Arg Gln Leu Pro Ser Phe Gln Thr Phe Phe Ala Pro Ala Leu Asp

Page 504

PH-1064PCT-US seq.TXT

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320

325

330

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Thr Pro Thr Pro Ser Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu

335

340

345

ccc acg aca gat ggg gcc cac cct caa cca ata tcc ccc atc cct ggt 1226

Pro Thr Thr Asp Gly Ala His Pro Gln Pro Ile Ser Pro Ile Pro Gly

350

355

360

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365

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Val Pro Ala Gln Ser Gln Ala Gly Ser Leu Val

380

385

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<211> 390

<212> PRT

<213> Homo sapiens

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Val Leu Pro Ala Trp Tyr Thr Leu His Gly Glu Val Ser Ser Ser Gln

50 55 60

Pro Trp Glu Val Pro Phe Val Met Trp Phe Phe Lys Gln Lys Glu Lys

65 70 75 80

Glu Asp Gln Val Leu Ser Tyr Ile Asn Gly Val Thr Thr Ser Lys Pro

85 90 95

Gly Val Ser Leu Val Tyr Ser Met Pro Ser Arg Asn Leu Ser Leu Arg

100 105 110

Leu Glu Gly Leu Gln Glu Lys Asp Ser Gly Pro Tyr Ser Cys Ser Val

115 120 125

Asn Val Gln Asp Lys Gln Gly Lys Ser Arg Gly His Ser Ile Lys Thr

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Leu Ser Leu Thr Asn Leu Ser Ser Ser Met Ala Gly Val Tyr Val Cys			
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Val Ser Thr Gly Pro Gly Ala Ala Val Val Ala Gly Ala Val Val Gly			
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Thr Leu Val Gly Leu Gly Leu Leu Ala Gly Leu Val Leu Leu Tyr His			
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Arg Arg Gly Lys Ala Leu Glu Glu Pro Ala Asn Asp Ile Lys Glu Asp			
	275	280	285
Ala Ile Ala Pro Arg Thr Leu Pro Trp Pro Lys Ser Ser Asp Thr Ile			
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Ser Lys Asn Gly Thr Leu Ser Ser Val Thr Ser Ala Arg Ala Leu Trp			
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Pro Pro His Gly Pro Pro Arg Pro Gly Ala Leu Thr Pro Thr Pro Ser			
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Leu Ser Ser Gln Ala Leu Pro Ser Pro Arg Leu Pro Thr Thr Asp Gly			
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PH-1064PCT-US seq.TXT

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360

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380

Gln Ala Gly Ser Leu Val

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390

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Met Lys Lys Gln Phe Asn Arg Met Lys Gln

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15

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25

gaa gat cta tta cag att gag aga cgc ctg gac acg gtg cgg tca ata 209

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gct caa aat atg caa gaa gca tcg act cag ctg gaa gac tct ctc ctg	353		
Ala Gln Asn Met Gln Glu Ala Ser Thr Gln Leu Glu Asp Ser Leu Leu			
75	80	85	90
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Gly Lys Met Leu Glu Thr Cys Gly Asp Ala Glu Asn Gln Leu Ala Leu			
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gag ctc tcc cag cac gaa gtc ttt gtt gag aag gag atc gtg gac cct	449		
Glu Leu Ser Gln His Glu Val Phe Val Glu Lys Glu Ile Val Asp Pro			
110	115	120	
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Leu Tyr Gly Ile Ala Glu Val Glu Ile Pro Asn Ile Gln Lys Gln Arg			
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aag cag ctt gca aga ttg gtg tta gac tgg gat tca gtc aga gcc agg	545		
Lys Gln Leu Ala Arg Leu Val Leu Asp Trp Asp Ser Val Arg Ala Arg			
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Val Glu Gln Cys Lys Asp Gln Leu Ala Ala Asp Met Tyr Asn Phe Met				
190	195	200		
gcc aaa gaa ggg gag tat ggc aaa ttc ttt gtt acg tta tta gaa gcc	737			
Ala Lys Glu Gly Glu Tyr Gly Lys Phe Phe Val Thr Leu Leu Glu Ala				
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caa gca gat tac cat aga aaa gca tta gca gtc tta gaa aag acc ctc	785			
Gln Ala Asp Tyr His Arg Lys Ala Leu Ala Val Leu Glu Lys Thr Leu				
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ccc gaa atg cga gcc cat caa gat aag tgg gcg gaa aaa cca gcc ttt	833			
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Gly Thr Pro Leu Glu Glu His Leu Lys Arg Ser Gly Arg Glu Ile Ala				
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ctg ccc att gaa gcc tgt gtc atg ctg ctt ctg gag aca ggc atg aag	929			
Leu Pro Ile Glu Ala Cys Val Met Leu Leu Leu Glu Thr Gly Met Lys				
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gag gag ggc ctt ttc cga att ggg gct ggg gcc tcc aag tta aag aag	977			
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Ser Asp Pro His Ala Val Ala Gly Ala Leu Lys Ser Tyr Leu Arg Glu			
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Leu Pro Glu Pro Leu Met Thr Phe Asn Leu Tyr Glu Glu Trp Thr Gln			
335	340	345	
gtt gca agt gtg cag gat caa gac aaa aaa ctt caa gac ttg tgg aga			1169
Val Ala Ser Val Gln Asp Gln Asp Lys Lys Leu Gln Asp Leu Trp Arg			
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Thr Cys Gln Lys Leu Pro Pro Gln Asn Phe Val Asn Phe Arg Tyr Leu			
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atc aag ttc ctt gca aag ctt gct cag acc agc gat gtg aat aaa atg			1265
Ile Lys Phe Leu Ala Lys Leu Ala Gln Thr Ser Asp Val Asn Lys Met			
380	385	390	
act ccc agc aac att gcg att gtg tta ggc cct aac ttg tta tgg gcc			1313
Thr Pro Ser Asn Ile Ala Ile Val Leu Gly Pro Asn Leu Leu Trp Ala			
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aga aat gaa gga aca ctt gct gaa atg gca gca gcc aca tcc gtc cat			1361
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Pro Glu Glu Val Glu Phe Asn Val Ser Glu Ala Phe Val Pro Leu Thr			
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Thr Pro Ser Ser Asn His Ser Phe His Thr Gly Asn Asp Ser Asp Ser			
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Gly Thr Leu Glu Arg Lys Arg Pro Ala Ser Met Ala Val Met Glu Gly			
475	480	485	490
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Asp Leu Val Lys Lys Glu Ser Phe Gly Val Lys Leu Met Asp Phe Gln			
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575 580 585
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590 595 600
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620 625 630
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Lys Pro Ala Pro Ala Pro Pro Lys Pro Gly Asn Pro Pro Pro Gly His
635 640 645 650
ccc ggg ggc cag agt tct tca gga aca tct cag cat cca ccc agt ctg 2081
Pro Gly Gly Gln Ser Ser Ser Gly Thr Ser Gln His Pro Pro Ser Leu
655 660 665
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Arg Arg Tyr Ser Ser Ser Leu Ser Pro Ile Gln Ala Pro Asn His Pro			
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                830                835                840
agg gtt tca gaa ccg cat cgc agc atc ttt cct gaa atg cac tca gac 2657
Arg Val Ser Glu Pro His Arg Ser Ile Phe Pro Glu Met His Ser Asp
                845                850                855
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                860                865                870
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Asp Thr Glu Ser Thr Ala Leu
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<210> 146

<211> 881

<212> PRT

<213> Homo sapiens

<400> 146

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Glu	Arg	Arg	Leu	Asp	Thr	Val	Arg	Ser	Ile	Cys	His	His	Ser	His	Lys
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Lys Glu Glu Met Asp Glu Ala Gly Asn Lys Val Glu Gln Cys Lys Asp		
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195	200	205
Gly Lys Phe Phe Val Thr Leu Leu Glu Ala Gln Ala Asp Tyr His Arg		
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Lys Ala Leu Ala Val Leu Glu Lys Thr Leu Pro Glu Met Arg Ala His		
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Cys Ser Thr Ser His Leu Asp Glu Phe Tyr Ser Asp Pro His Ala Val		

PH-1064PCT-US seq.TXT

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Gln	Asp	Lys	Lys	Leu	Gln	Asp	Leu	Trp	Arg	Thr	Cys	Gln	Lys	Leu	Pro
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Ala	Glu	Met	Ala	Ala	Ala	Thr	Ser	Val	His	Val	Val	Ala	Val	Ile	Glu
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Arg	Pro	Ala	Ser	Met	Ala	Val	Met	Glu	Gly	Asp	Leu	Val	Lys	Lys	Glu
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Gly Ser His Gln Leu Ser Met Gly Gln Pro His Asn Ala Ala Gly Pro		
610	615	620
Ser Pro His Thr Leu Arg Arg Ala Val Lys Lys Pro Ala Pro Ala Pro		
625	630	635
Pro Lys Pro Gly Asn Pro Pro Pro Gly His Pro Gly Gly Gln Ser Ser		
645	650	655
Ser Gly Thr Ser Gln His Pro Pro Ser Leu Ser Pro Lys Pro Pro Thr		
660	665	670
Arg Ser Pro Ser Pro Pro Thr Gln His Thr Gly Gln Pro Pro Gly Gln		
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PH-1064PCT-US seq.TXT

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725	730	735
Asn Pro Met Ala Leu Pro	Ser Glu His Gly Leu Glu	Gln Pro Ser His
740	745	750
Thr Pro Pro Gln Thr Pro	Thr Pro Pro Ser Thr Pro	Pro Leu Gly Lys
755	760	765
Gln Asn Pro Ser Leu Pro	Ala Pro Gln Thr Leu Ala	Gly Gly Asn Pro
770	775	780
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785	790	795
Pro Lys Pro Arg Asn Arg	Pro Ser Val Pro Pro Pro	Pro Gln Pro Pro
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Ala Ser Lys Ile Val Thr	Asp Ser Asn Ser Arg Val	Ser Glu Pro His
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Arg Ser Ile Phe Pro Glu	Met His Ser Asp Ser Ala	Ser Lys Asp Val
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<211> 3021

<212> DNA

<213> Homo sapiens

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<222> (140)..(1105)

<400> 147

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Thr Thr Thr Thr Ser Ser Ser Gly Leu Gly Ser Pro Met Ile Val Gly
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PH-1064PCT-US seq.TXT

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Phe	Ser	Val	Thr	Leu	Ile	Ile	Leu	Ile	Val	Glu	Leu	Cys	Gly	Leu	Gln	
				80					85					90		
gcc	cgc	ttc	ccc	ctg	tct	tgg	cgc	aac	ttc	ccc	atc	acc	ttc	gcc	tgc	460
Ala	Arg	Phe	Pro	Leu	Ser	Trp	Arg	Asn	Phe	Pro	Ile	Thr	Phe	Ala	Cys	
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tat	gcg	ggc	ctc	ttc	tgc	ctc	tcg	gcc	tcc	atc	atc	tac	ccc	acc	acc	508
Tyr	Ala	Gly	Leu	Phe	Cys	Leu	Ser	Ala	Ser	Ile	Ile	Tyr	Pro	Thr	Thr	
	110						115					120				
tat	gtc	cag	ttc	ctg	tcc	cac	ggc	cgt	tcg	cgg	gac	cac	gcc	atc	gcc	556
Tyr	Val	Gln	Phe	Leu	Ser	His	Gly	Arg	Ser	Arg	Asp	His	Ala	Ile	Ala	
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gcc	acc	ttc	ttc	tcc	tgc	atc	gcg	tgt	gtg	gct	tac	gcc	acc	gaa	gtg	604
Ala	Thr	Phe	Phe	Ser	Cys	Ile	Ala	Cys	Val	Ala	Tyr	Ala	Thr	Glu	Val	
140					145					150				155		
gcc	tgg	acc	cgg	gcc	cgg	ccc	ggc	gag	atc	act	ggc	tat	atg	gcc	acc	652
Ala	Trp	Thr	Arg	Ala	Arg	Pro	Gly	Glu	Ile	Thr	Gly	Tyr	Met	Ala	Thr	
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gta	ccc	ggg	ctg	ctg	aag	gtg	ctg	gag	acc	ttc	gtt	gcc	tgc	atc	atc	700
Val	Pro	Gly	Leu	Leu	Lys	Val	Leu	Glu	Thr	Phe	Val	Ala	Cys	Ile	Ile	
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PH-1064PCT-US seq.TXT

Phe	Ala	Phe	Ile	Ser	Asp	Pro	Asn	Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu		
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gag	tgg	tgc	gtg	gcg	gtg	tac	gcc	atc	tgc	ttc	atc	cta	gcg	gcc	atc	796	
Glu	Trp	Cys	Val	Ala	Val	Tyr	Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile		
		205						210						215			
gcc	atc	ctg	ctg	aac	ctg	ggg	gag	tgc	acc	aac	gtg	cta	ccc	atc	ccc	844	
Ala	Ile	Leu	Leu	Asn	Leu	Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro		
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Phe	Pro	Ser	Phe	Leu	Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr		
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ggc	ggc	cag	cct	cgg	cgc	tcg	aga	gat	gta	agc	tgc	agc	cgc	agc	cat	988	
Gly	Gly	Gln	Pro	Arg	Arg	Ser	Arg	Asp	Val	Ser	Cys	Ser	Arg	Ser	His		
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PH-1064PCT-US seq.TXT
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320

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PH-1064PCT-US seq.TXT

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<210> 148

<211> 322

<212> PRT

<213> Homo sapiens

<400> 148

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Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp Thr Gly Ser Met
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PH-1064PCT-US seq.TXT

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Ser	His	Gly	Arg	Ser	Arg	Asp	His	Ala	Ile	Ala	Ala	Thr	Phe	Phe	Ser
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Cys	Ile	Ala	Cys	Val	Ala	Tyr	Ala	Thr	Glu	Val	Ala	Trp	Thr	Arg	Ala
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Arg	Pro	Gly	Glu	Ile	Thr	Gly	Tyr	Met	Ala	Thr	Val	Pro	Gly	Leu	Leu
		165		170		175									
Lys	Val	Leu	Glu	Thr	Phe	Val	Ala	Cys	Ile	Ile	Phe	Ala	Phe	Ile	Ser
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Asp	Pro	Asn	Leu	Tyr	Gln	His	Gln	Pro	Ala	Leu	Glu	Trp	Cys	Val	Ala
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Val	Tyr	Ala	Ile	Cys	Phe	Ile	Leu	Ala	Ala	Ile	Ala	Ile	Leu	Leu	Asn
		210		215		220									
Leu	Gly	Glu	Cys	Thr	Asn	Val	Leu	Pro	Ile	Pro	Phe	Pro	Ser	Phe	Leu
225				230				235						240	
Ser	Gly	Leu	Ala	Leu	Leu	Ser	Val	Leu	Leu	Tyr	Ala	Thr	Ala	Leu	Val
		245		250		255									
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<210> 149

<211> 4409

<212> DNA

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<222> (39)..(2027)

<400> 149

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Ser Gln Gly Val Val Leu Thr Ala Tyr His Pro Ser Gly Lys Asp Gln

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15

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PH-1064PCT-US seq.TXT

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Arg	Arg	Tyr	Gly	Gln	Tyr	Thr	Met	Asn	Gln	Glu	Ser	Thr	Thr	Ile	Lys		
	40						45					50					
gtt	atg	gag	aag	cct	cca	ttt	gat	cga	tca	att	tcc	cag	gat	tct	ttg	248	
Val	Met	Glu	Lys	Pro	Pro	Phe	Asp	Arg	Ser	Ile	Ser	Gln	Asp	Ser	Leu		
	55					60					65				70		
gat	gaa	cta	tct	atg	gaa	gac	tat	tgg	ata	gaa	cta	gaa	aac	atc	aag	296	
Asp	Glu	Leu	Ser	Met	Glu	Asp	Tyr	Trp	Ile	Glu	Leu	Glu	Asn	Ile	Lys		
					75					80					85		
aaa	tct	agt	gaa	aac	agc	caa	gaa	gat	caa	gag	gtg	gtt	gtt	gtc	aaa	344	
Lys	Ser	Ser	Glu	Asn	Ser	Gln	Glu	Asp	Gln	Glu	Val	Val	Val	Val	Lys		
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gag	cct	gat	gag	gga	gaa	ttg	gaa	gaa	gag	tgg	ctt	aaa	gag	gcc	ggt	392	
Glu	Pro	Asp	Glu	Gly	Glu	Leu	Glu	Glu	Glu	Trp	Leu	Lys	Glu	Ala	Gly		
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tta	tcc	aat	ctc	ttc	gga	gag	tct	gct	gga	gat	cca	cag	gaa	agc	att	440	
Leu	Ser	Asn	Leu	Phe	Gly	Glu	Ser	Ala	Gly	Asp	Pro	Gln	Glu	Ser	Ile		
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gtg	ttt	tta	tca	aca	ttg	acg	cgg	acc	cag	gca	gca	gca	gtt	cag	aag	488	
Val	Phe	Leu	Ser	Thr	Leu	Thr	Arg	Thr	Gln	Ala	Ala	Ala	Val	Gln	Lys		
					135					140					145		
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PH-1064PCT-US seq.TXT

Arg	Val	Glu	Thr	Val	Ser	Gln	Thr	Leu	Arg	Lys	Lys	Asn	Lys	Gln	Tyr	
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Gln	Ile	Pro	Asp	Val	Arg	Asp	Ile	Phe	Ala	Gln	Gln	Arg	Glu	Ser	Lys	
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Glu	Thr	Ala	Pro	Gly	Gly	Thr	Glu	Ser	Gln	Ser	Leu	Arg	Thr	Asn	Glu	
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Asn	Lys	Tyr	Gln	Gly	Arg	Asp	Asp	Glu	Ala	Ser	Asn	Leu	Val	Gly	Glu	
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gag	aag	ctg	atc	cca	cct	gag	gag	acg	cct	gcc	cct	gaa	aca	gac	atc	728
Glu	Lys	Leu	Ile	Pro	Pro	Glu	Glu	Thr	Pro	Ala	Pro	Glu	Thr	Asp	Ile	
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Asn	Leu	Glu	Val	Ser	Phe	Ala	Glu	Gln	Ala	Leu	Asn	Gln	Lys	Glu	Ser	
				235				240						245		
tcc	aag	gag	aaa	atc	cag	aag	agc	aaa	ggc	gat	gat	gcc	aca	tta	cct	824
Ser	Lys	Glu	Lys	Ile	Gln	Lys	Ser	Lys	Gly	Asp	Asp	Ala	Thr	Leu	Pro	
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agt	ttc	aga	ttg	cca	aaa	gac	aaa	acg	ggg	acc	aca	agg	att	ggg	gac	872
Ser	Phe	Arg	Leu	Pro	Lys	Asp	Lys	Thr	Gly	Thr	Thr	Arg	Ile	Gly	Asp	
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PH-1064PCT-US seq.TXT

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 295 300 305 310
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 Ala Val Lys Ile Lys Thr Lys Asp Ser Gly Leu Phe Cys Val Pro Leu
 315 320 325
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 330 335 340
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 345 350 355
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 Glu Thr Glu Gly Leu Leu Arg Ile Pro Gly Ala Ala Ile Arg Ile Lys
 360 365 370
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 Asn Leu Cys Gln Glu Leu Glu Ala Lys Phe Tyr Glu Gly Thr Phe Asn
 375 380 385 390
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 Trp Glu Ser Val Lys Gln His Asp Ala Ala Ser Leu Leu Lys Leu Phe
 395 400 405
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PH-1064PCT-US seq.TXT

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425	430	435
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Leu Asn Leu Leu Gly Ile Leu Leu Pro Asp Ala Asn Arg Asp Thr Leu		
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Lys Ala Leu Leu Glu Phe Leu Gln Arg Val Ile Asp Asn Lys Glu Lys		
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aat aaa atg aca gtc atg aat gta gca atg gtc atg gcc ccg aat ctc		1496
Asn Lys Met Thr Val Met Asn Val Ala Met Val Met Ala Pro Asn Leu		
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Gln Lys Leu Leu Trp Thr Ile Pro Lys Phe Ile Val Asn Gln Val Arg		
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PH-1064PCT-US seq.TXT

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PH-1064PCT-US seq.TXT

Leu

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caagaaaata ggactgtcag aagctgccag ttattactga accattaaat acttatatac 2737
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<210> 150

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<212> PRT

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Ala Glu Pro Pro Val Arg Arg Asp Asn Pro Phe Phe Arg Ser Lys Arg
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Asp Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile	
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Cys Ser Ile Ser Pro Val Leu Glu Val Lys Leu Ser Asn Leu Glu Val	
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 Glu Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg
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PH-1064PCT-US seq.TXT

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PH-1064PCT-US seq.TXT

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Ser Ser Gly Gly Ala Val Gln Leu Pro Asp Thr Ser Ile Ser Ile His		
225	230	235
Val Pro Glu Gly His Val Ala Pro Gly Glu Thr Gln Gln Ile Ser Met		
245	250	255
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275	280	285
Thr Ser Ile Ile Leu Glu Met Lys Val Ser Ala Glu Ile Lys Asn Asp		
290	295	300
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325	330	335
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His Pro Ser Phe Lys Thr Val Val Thr Ile Phe Gly His Asp Cys Ala		
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Pro Lys Thr Leu Leu Val Ser Glu Val Thr Arg Gln Ala Pro Asn Pro		400
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Ala Pro Val Ala Leu Gln Leu Trp Gly Lys His Gln Phe Val Leu Ser		415
	420	425
Arg Pro Gln Asp Leu Lys Val Cys Met Phe Ser Asn Met Thr Asn Tyr		430
	435	440
Glu Val Lys Ala Ser Glu Gln Ala Lys Val Val Arg Gly Phe Gln Leu		445
	450	455
Lys Leu Gly Lys Val Ser Arg Leu Ile Phe Pro Ile Thr Ser Gln Asn		460
465	470	475
Pro Asn Glu Leu Ser Asp Phe Thr Leu Arg Val Gln Val Lys Asp Asp		480
	485	490
Gln Glu Ala Ile Leu Thr Gln Phe Cys Val Gln Thr Pro Gln Pro Pro		495
	500	505
Pro Lys Ser Ala Ile Lys Pro Ser Gly Gln Arg Arg Phe Leu Lys Lys		510
	515	520
Asn Glu Val Gly Lys Ile Ile Leu Ser Pro Phe Ala Thr Thr Thr Lys		525
	530	535
Tyr Pro Thr Phe Gln Asp Arg Pro Val Ser Ser Leu Lys Phe Gly Lys		540
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Leu Leu Lys Thr Val Val Arg Gln Asn Lys Asn His Tyr Leu Leu Glu		560

PH-1064PCT-US seq.TXT

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Gly Arg Val Gly Leu Val His Thr Lys Asn Val Leu Val Val Gly Arg		
610	615	620
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625	630	635
Leu Glu Gln Ile Leu Arg Pro Cys Lys Phe Leu Thr Tyr Ile Tyr Ala		
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Ser Val Arg Thr Leu Leu Met Glu Asn Ile Ser Ser Trp Arg Ser Phe		
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Ala Asp Ala Leu Gly Tyr Val Asn Leu Pro Leu Thr Phe Phe Cys Arg		
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Ala Glu Leu Asp Ser Glu Pro Glu Arg Val Ala Ser Val Leu Glu Lys		
690	695	700
Leu Lys Glu Asp Cys Asn Asn Thr Glu Asn Lys Glu Arg Lys Ser Phe		
705	710	715
Gln Lys Glu Leu Val Met Ala Leu Leu Lys Met Asp Cys Gln Gly Leu		
725	730	735
Val Val Arg Leu Ile Gln Asp Phe Val Leu Leu Thr Thr Ala Val Glu		
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Thr Trp Ser His Gln Ile Gly Asp Ser Tyr Arg Asp Val Ile Gln Glu		
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Leu His Leu Gly Leu Asp Lys Met Lys Asn Pro Ile Thr Lys Arg Trp		
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Lys His Leu Thr Gly Thr Leu Ile Leu Val Asn Ser Leu Asp Val Leu		
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<213> Homo sapiens

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Phe Ser Phe Leu Leu Leu Val Leu Leu Leu Val Thr Arg Ser Pro Val

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Asn Ala Cys Leu Leu Thr Gly Ser Leu Phe Val Leu Leu Arg Val Phe

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agc ttt gag ccg gtg ccc tct tgc agg gcc ctg cag gtg ctc aag ccc 315

Ser Phe Glu Pro Val Pro Ser Cys Arg Ala Leu Gln Val Leu Lys Pro

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Arg Asp Arg Ile Ser Ala Ile Ala His Arg Gly Gly Ser His Asp Ala

65 70 75

ccc gag aac acg ctg gcg gcc att cgg cag gca gct aag aat gga gca 411

Pro Glu Asn Thr Leu Ala Ala Ile Arg Gln Ala Ala Lys Asn Gly Ala

80 85 90

aca ggc gtg gag ttg gac att gag ttt act tct gac ggg att cct gtc 459

Thr Gly Val Glu Leu Asp Ile Glu Phe Thr Ser Asp Gly Ile Pro Val

95 100 105

tta atg cac gat aac aca gta gat agg acg act gat ggg act ggg cga 507

Leu Met His Asp Asn Thr Val Asp Arg Thr Thr Asp Gly Thr Gly Arg

110 115 120 125

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aac cac aga ctc agg aat gat ttc cct gat gaa aag atc cct acc cta 603
Asn His Arg Leu Arg Asn Asp Phe Pro Asp Glu Lys Ile Pro Thr Leu
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agg gaa gct gtt gca gag tgc cta aac cat aac ctc aca atc ttc ttt 651
Arg Glu Ala Val Ala Glu Cys Leu Asn His Asn Leu Thr Ile Phe Phe
      160              165              170
gat gtc aaa ggc cat gca cac aag gct act gag gct cta aag aaa atg 699
Asp Val Lys Gly His Ala His Lys Ala Thr Glu Ala Leu Lys Lys Met
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tat atg gaa ttt cct caa ctg tat aat aat agt gtg gtc tgt tct ttc 747
Tyr Met Glu Phe Pro Gln Leu Tyr Asn Asn Ser Val Val Cys Ser Phe
      190              195              200              205
ttg cca gaa gtt atc tac aag atg aga caa aca gat cgg gat gta ata 795
Leu Pro Glu Val Ile Tyr Lys Met Arg Gln Thr Asp Arg Asp Val Ile
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aca gca tta act cac aga cct tgg agc cta agc cat aca gga gat ggg 843
Thr Ala Leu Thr His Arg Pro Trp Ser Leu Ser His Thr Gly Asp Gly
      225              230              235
aaa cca cgc tat gat act ttc tgg aaa cat ttt ata ttt gtt atg atg 891
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 Gly Ile Ser Ala Phe Leu Met Gln Lys Asp Phe Val Ser Pro Ala Tyr
 270 275 280 285

ttg aag aag tgg tca gct aaa gga atc cag gtt gtt ggt tgg act gtt 1035
 Leu Lys Lys Trp Ser Ala Lys Gly Ile Gln Val Val Gly Trp Thr Val
 290 295 300

aat acc ttt gat gaa aag agt tac tac gaa tcc cat ctt ggt tcc agc 1083
 Asn Thr Phe Asp Glu Lys Ser Tyr Tyr Glu Ser His Leu Gly Ser Ser
 305 310 315

tat atc act gac agc atg gta gaa gac tgc gaa cct cac ttc 1125
 Tyr Ile Thr Asp Ser Met Val Glu Asp Cys Glu Pro His Phe
 320 325 330

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PH-1064PCT-US seq.TXT

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<210> 154

<211> 331

<212> PRT

<213> Homo sapiens

<400> 154

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		35						40					45		
Pro	Val	Pro	Ser	Cys	Arg	Ala	Leu	Gln	Val	Leu	Lys	Pro	Arg	Asp	Arg
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PH-1064PCT-US seq.TXT

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Leu	Thr	Phe	Glu	Gln	Ile	Arg	Lys	Leu	Asn	Pro	Ala	Ala	Asn	His	Arg
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Val	Ile	Tyr	Lys	Met	Arg	Gln	Thr	Asp	Arg	Asp	Val	Ile	Thr	Ala	Leu
									210						220
Thr	His	Arg	Pro	Trp	Ser	Leu	Ser	His	Thr	Gly	Asp	Gly	Lys	Pro	Arg
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Tyr	Asp	Thr	Phe	Trp	Lys	His	Phe	Ile	Phe	Val	Met	Met	Asp	Ile	Leu
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PH-1064PCT-US seq.TXT

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<212> DNA

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Asp His Ile Arg Asp Leu Asp Val Val Val Val Ser Val Ala Gly Ala
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Phe Arg Lys Gly Lys Ser Phe Ile Leu Asp Phe Met Leu Arg Tyr Leu
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tat tct cag aag gaa agt ggc cat tca aat tgg ttg ggt gac cca gaa 343

Tyr Ser Gln Lys Glu Ser Gly His Ser Asn Trp Leu Gly Asp Pro Glu
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gaa ccg tta aca gga ttt tcc tgg aga ggg gga tct gat cca gaa acc 391

Glu Pro Leu Thr Gly Phe Ser Trp Arg Gly Gly Ser Asp Pro Glu Thr
      105                      110                      115

act ggg att caa atc tgg agt gaa gtt ttc act gtg gag aag cca ggt 439

Thr Gly Ile Gln Ile Trp Ser Glu Val Phe Thr Val Glu Lys Pro Gly
      120                      125                      130

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Ser Gln Ser Thr Val Lys Asp Cys Ala Thr Ile Phe Ala Leu Ser Thr
      150                      155                      160

atg act agt tct gtt cag att tat aat tta tct cag aac att caa gaa      583

Met Thr Ser Ser Val Gln Ile Tyr Asn Leu Ser Gln Asn Ile Gln Glu
      165                      170                      175                      180

gat gat ctt caa cag ctg cag ctc ttc aca gaa tac ggt cgt ctg gca      631

Asp Asp Leu Gln Gln Leu Gln Leu Phe Thr Glu Tyr Gly Arg Leu Ala
      185                      190                      195

atg gat gaa att ttc caa aag cct ttc cag aca ctg atg ttt ttg gtt      679

Met Asp Glu Ile Phe Gln Lys Pro Phe Gln Thr Leu Met Phe Leu Val
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aga gat tgg agt ttc cct tat gaa tat agc tat gga ctc caa gga gga      727

Arg Asp Trp Ser Phe Pro Tyr Glu Tyr Ser Tyr Gly Leu Gln Gly Gly
      215                      220                      225

atg gca ttt ttg gat aag cgt tta cag gtg aag gaa cat caa cat gaa      775

Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu His Gln His Glu

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acc tgc ttt ctc tta cca cat cca gga ctc cag gtg gcc aca agc cct      871

Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val Ala Thr Ser Pro
                                265                                270                                275
gac ttt gat ggg aaa tta aaa gat att gct ggt gaa ttc aaa gag cag      919

Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu Phe Lys Glu Gln
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tta cag gca ctg ata ccg tat gta tta aac cca tct aag tta atg gaa      967

Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser Lys Leu Met Glu
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aag gag atc aat ggc tca aag gtc acc tgt cgg gga cta ctg gag tat      1015

Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly Leu Leu Glu Tyr
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ttt aag gca tat att aaa att tat caa gga gaa gat ctg cct cac ccc      1063

Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp Leu Pro His Pro
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375	380	385	
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PH-1064PCT-US seq.TXT

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ctc acc tgg ggc tac atc agg tat tct ggt caa tat cgt gag ctg ggc	1543
Leu Thr Trp Gly Tyr Ile Arg Tyr Ser Gly Gln Tyr Arg Glu Leu Gly	
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<213> Homo sapiens

<400> 156

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PH-1064PCT-US seq.TXT

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Leu	Arg	Tyr	Leu	Tyr	Ser	Gln	Lys	Glu	Ser	Gly	His	Ser	Asn	Trp	Leu
				85					90					95	
Gly	Asp	Pro	Glu	Glu	Pro	Leu	Thr	Gly	Phe	Ser	Trp	Arg	Gly	Gly	Ser
		100						105					110		
Asp	Pro	Glu	Thr	Thr	Gly	Ile	Gln	Ile	Trp	Ser	Glu	Val	Phe	Thr	Val
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Glu	Lys	Pro	Gly	Gly	Lys	Lys	Val	Ala	Val	Val	Leu	Met	Asp	Thr	Gln
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Ala	Leu	Ser	Thr	Met	Thr	Ser	Ser	Val	Gln	Ile	Tyr	Asn	Leu	Ser	Gln
				165					170				175		
Asn	Ile	Gln	Glu	Asp	Asp	Leu	Gln	Gln	Leu	Gln	Leu	Phe	Thr	Glu	Tyr
		180						185				190			
Gly	Arg	Leu	Ala	Met	Asp	Glu	Ile	Phe	Gln	Lys	Pro	Phe	Gln	Thr	Leu
		195						200				205			
Met	Phe	Leu	Val	Arg	Asp	Trp	Ser	Phe	Pro	Tyr	Glu	Tyr	Ser	Tyr	Gly
	210						215					220			

PH-1064PCT-US seq.TXT

Leu Gln Gly Gly Met Ala Phe Leu Asp Lys Arg Leu Gln Val Lys Glu
 225 230 235 240
 His Gln His Glu Glu Ile Gln Asn Val Arg Asn His Ile His Ser Cys
 245 250 255
 Phe Ser Asp Val Thr Cys Phe Leu Leu Pro His Pro Gly Leu Gln Val
 260 265 270
 Ala Thr Ser Pro Asp Phe Asp Gly Lys Leu Lys Asp Ile Ala Gly Glu
 275 280 285
 Phe Lys Glu Gln Leu Gln Ala Leu Ile Pro Tyr Val Leu Asn Pro Ser
 290 295 300
 Lys Leu Met Glu Lys Glu Ile Asn Gly Ser Lys Val Thr Cys Arg Gly
 305 310 315 320
 Leu Leu Glu Tyr Phe Lys Ala Tyr Ile Lys Ile Tyr Gln Gly Glu Asp
 325 330 335
 Leu Pro His Pro Lys Ser Met Leu Gln Ala Thr Ala Glu Ala Asn Asn
 340 345 350
 Leu Ala Ala Ala Ala Ser Ala Lys Asp Ile Tyr Tyr Asn Asn Met Glu
 355 360 365
 Glu Val Cys Gly Gly Glu Lys Pro Tyr Leu Ser Pro Asp Ile Leu Glu
 370 375 380
 Glu Lys His Cys Glu Phe Lys Gln Leu Ala Leu Asp His Phe Lys Lys
 385 390 395 400
 Thr Lys Lys Met Gly Gly Lys Asp Phe Ser Phe Arg Tyr Gln Gln Glu
 405 410 415

PH-1064PCT-US seq.TXT

Leu	Glu	Glu	Glu	Ile	Lys	Glu	Leu	Tyr	Glu	Asn	Phe	Cys	Lys	His	Asn
			420					425						430	
Gly	Ser	Lys	Asn	Val	Phe	Ser	Thr	Phe	Arg	Thr	Pro	Ala	Val	Leu	Phe
			435					440						445	
Thr	Gly	Ile	Val	Ala	Leu	Tyr	Ile	Ala	Ser	Gly	Leu	Thr	Gly	Phe	Ile
			450					455						460	
Gly	Leu	Glu	Val	Val	Ala	Gln	Leu	Phe	Asn	Cys	Met	Val	Gly	Leu	Leu
465						470					475				480
Leu	Ile	Ala	Leu	Leu	Thr	Trp	Gly	Tyr	Ile	Arg	Tyr	Ser	Gly	Gln	Tyr
					485					490				495	
Arg	Glu	Leu	Gly	Gly	Ala	Ile	Asp	Phe	Gly	Ala	Ala	Tyr	Val	Leu	Glu
					500					505				510	
Gln	Ala	Ser	Ser	His	Ile	Gly	Asn	Ser	Thr	Gln	Ala	Thr	Val	Arg	Asp
					515					520				525	
Ala	Val	Val	Gly	Arg	Pro	Ser	Met	Asp	Lys	Lys	Ala	Gln			
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<210> 157

<211> 2172

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (45) .. (563)

<400> 157

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ccg ggc gac ccg cgg caa ccc cac cgc ccc gac ccc ggc cgc cca gtg 104

Pro Gly Asp Pro Arg Gln Pro His Arg Pro Asp Pro Gly Arg Pro Val
   5              10              15              20

ggc ctg gag cag ctg cgg cgg ctc ggg gtg ctc tac tgg aag ctg gat 152

Gly Leu Glu Gln Leu Arg Arg Leu Gly Val Leu Tyr Trp Lys Leu Asp
          25              30              35

gct gac aaa tat gag aat gat cca gaa tta gaa aag atc cga aga gag 200

Ala Asp Lys Tyr Glu Asn Asp Pro Glu Leu Glu Lys Ile Arg Arg Glu
          40              45              50

agg aac tac tcc tgg atg gac atc ata acc ata tgc aaa gat aaa cta 248

Arg Asn Tyr Ser Trp Met Asp Ile Ile Thr Ile Cys Lys Asp Lys Leu
          55              60              65

cca aat tat gaa gaa aag att aag atg ttc tac gag gag cat ttg cac 296

Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu Glu His Leu His
          70              75              80

ttg gac gat gag atc cgc tac atc ctg gat ggc agt ggg tac ttc gat 344

Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser Gly Tyr Phe Asp

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PH-1064PCT-US seq.TXT

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gtg agg gac aag gag gac cag tgg atc cgg atc ttc atg gag aag gga				392
Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe Met Glu Lys Gly				
	105	110	115	
gac atg gtg acg ctc ccc gcg ggg atc tat cac cgc ttc acg gtg gac				440
Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg Phe Thr Val Asp				
	120	125	130	
gag aag aac tac acg aag gcc atg cgg ctg ttt gtg gga gaa ccg gtg				488
Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val Gly Glu Pro Val				
	135	140	145	
tgg aca gcg tac aac cgg ccc gct gac cat ttt gaa gcc cgc ggg cag				536
Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu Ala Arg Gly Gln				
	150	155	160	
tac gtg aaa ttt ctg gca cag acc gcc tagcagtgcgc gcctgggaac				583
Tyr Val Lys Phe Leu Ala Gln Thr Ala				
165	170			
taacacgtgc ctcgtaaagg tccccaatgt aatgactgag cagaaaatca atcactttct				643
ctttgctttt agaggatagc cttgaggcta gattatcttt cctttgtaag attatttgat				703
cagaatattt tgtaatgaaa ggatctagaa agcaacttgg aagtgtaaag agtcaccttc				763
attttctgta actcaatcaa gactgggtggg tccatggccc tgtgttagtt catgcattca				823

PH-1064PCT-US seq.TXT

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cgtgatgccg cgcctgccgt gtaagaaggt gcaatcctag ataacacagc tagccagata 943
gaagacactt ttttctccaa aatgatgcct tgggggtgggg agtggtaggg ggaagagctc 1003
ccaccctaag gggcacacac tgagttgctt atgccacttc ctgtttcaaa ataaagtaac 1063
tgccttaatc ttatactcat ggcttggagt taccttatat tcaggtatat gtgatatttt 1123
gcctggtttg ttaaaattgc cccatttaga ttccttctat aattgttctt atagataagt 1183
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ggattaatth tcttaatcac ctccacactg tacagaggaa actcaagcct taaatgttta 1483
agtaaactct gtctcagttt taggattaaa ataccaccg gtgggtgtgat gatgccatat 1543
accgcagggc ttgcttctgt caagtgtgac tctatctcag taattaaaat aagtgtgat 1603
ctactgattt tttttaatgg attcatttct aatggggcat tataaataga gcttgttcat 1663
ttttaagaac gaaacattca tatgataaac tatcgcttta aattgccttt ctgcttcat 1723
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PH-1064PCT-US seq.TXT

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 caggaggcta aggtgggagg attcttagag cctgggaggt cgaggctgca gtgagctgtg 1963
 attgtggcca ctgcactcca gcctgggtga cagagcgaga ctctgtctca aaaaagaaga 2023
 aagagtaaga gctgaggcat ataatagaat tctgctaaag cacttaaggt gaaatcacat 2083
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 ataaaatgta ctcattttca gtgtttttg 2172

<210> 158

<211> 173

<212> PRT

<213> Homo sapiens

<400> 158

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Gly	Arg	Pro	Val	Gly	Leu	Glu	Gln	Leu	Arg	Arg	Leu	Gly	Val	Leu	Tyr
				20					25					30	
Trp	Lys	Leu	Asp	Ala	Asp	Lys	Tyr	Glu	Asn	Asp	Pro	Glu	Leu	Glu	Lys
				35					40					45	
Ile	Arg	Arg	Glu	Arg	Asn	Tyr	Ser	Trp	Met	Asp	Ile	Ile	Thr	Ile	Cys

PH-1064PCT-US seq.TXT

50	55	60
Lys Asp Lys Leu Pro Asn Tyr Glu Glu Lys Ile Lys Met Phe Tyr Glu		
65	70	75
Glu His Leu His Leu Asp Asp Glu Ile Arg Tyr Ile Leu Asp Gly Ser		
	85	90
Gly Tyr Phe Asp Val Arg Asp Lys Glu Asp Gln Trp Ile Arg Ile Phe		
	100	105
Met Glu Lys Gly Asp Met Val Thr Leu Pro Ala Gly Ile Tyr His Arg		
	115	120
Phe Thr Val Asp Glu Lys Asn Tyr Thr Lys Ala Met Arg Leu Phe Val		
	130	135
Gly Glu Pro Val Trp Thr Ala Tyr Asn Arg Pro Ala Asp His Phe Glu		
145	150	155
Ala Arg Gly Gln Tyr Val Lys Phe Leu Ala Gln Thr Ala		
	165	170

<210> 159

<211> 20

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 159

ggaagtgtta cttctgctct

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<210> 160

<211> 50

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 160

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<210> 161

<211> 41

<212> DNA

<220>

<223> Description of the artificial sequence:an artificially synthesized primer sequence

<400> 161

gagagagaga gagagagcgg ccgcactagt cccccccccc c 41

<210> 162

<211> 30

<212> RNA

<213> Artificial Sequence

<220>

<223> Description of the artificial sequence: an artificially synthesized oligo-cap linker sequence

<400> 162

agcaucgagu cggccuuguu ggccuacugg 30

<210> 163

<211> 42

<212> DNA

<213> Artificial Sequence

PH-1064PCT-US seq.TXT

<220>
 <223> Description of the artificial sequence: an artificially synthesized oligo(dT)primer sequence
 <400> 163
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<210> 164
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<210> 165
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<210> 166
 <211> 30
 <212> DNA
 <213> Artificial Sequence
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 <400> 166
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PH-1064PCT-US seq.TXT

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222>(139)..(1062)

<400> 168

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120

CCTCCATTTC AGCTAATC ATG GGA GAG ATT AAA GTC TCT CCT GAT TAT AAC
171

Met Gly Glu Ile Lys Val Ser Pro Asp Tyr Asn

1

5

10

TGG TTT AGA GGT ACA GTT CCC CTT AAA AAG ATT ATT GTG GAT GAT GAT
219

Trp Phe Arg Gly Thr Val Pro Leu Lys Lys Ile Ile Val Asp Asp Asp

15

20

25

GAC AGT AAG ATA TGG TCG CTC TAT GAC GCG GGC CCC CGA AGT ATC AGG
267

Asp Ser Lys Ile Trp Ser Leu Tyr Asp Ala Gly Pro Arg Ser Ile Arg

30

35

40

TGT CCT CTC ATA TTC CTG CCC CCT GTC AGT GGA ACT GCA GAT GTC TTT
315

Cys Pro Leu Ile Phe Leu Pro Pro Val Ser Gly Thr Ala Asp Val Phe

45

50

55

TTC CGG CAG ATT TTG GCT CTG ACT GGA TGG GGT TAC CGG GTT ATC GCT
363

Phe Arg Gln Ile Leu Ala Leu Thr Gly Trp Gly Tyr Arg Val Ile Ala

60

65

70

75

TTG CAG TAT CCA GTT TAT TGG GAC CAT CTC GAG TTC TGT GAT GGA TTC
411

Leu Gln Tyr Pro Val Tyr Trp Asp His Leu Glu Phe Cys Asp Gly Phe

PH-1064PCT-US seq.TXT

	80		85		90
AGA AAA CTT TTA GAC CAT TTA CAA TTG GAT AAA GTT CAT CTT TTT GGC					
459					
Arg Lys Leu Leu Asp His Leu Gln Leu Asp Lys Val His Leu Phe Gly					
	95		100		105
GCT TCT TTG GGA GGC TTT TTG GCC CAG AAA TTT GCT GAA TAT ACT CAC					
507					
Ala Ser Leu Gly Gly Phe Leu Ala Gln Lys Phe Ala Glu Tyr Thr His					
	110		115		120
AAA TCT CCT AGA GTC CAT TCC CTA ATC CTC TGC AAT TCC TTC AGT GAC					
555					
Lys Ser Pro Arg Val His Ser Leu Ile Leu Cys Asn Ser Phe Ser Asp					
	125		130		135
ACC TCT ATC TTC AAC CAA ACT TGG ACT GCA AAC AGC TTT TGG CTG ATG					
603					
Thr Ser Ile Phe Asn Gln Thr Trp Thr Ala Asn Ser Phe Trp Leu Met					
	140		145		150
					155
CCT GCA TTT ATG CTC AAA AAA ATA GTT CTT GGA AAT TTT TCA TCT GGC					
651					
Pro Ala Phe Met Leu Lys Lys Ile Val Leu Gly Asn Phe Ser Ser Gly					
	160		165		170
CCG GTG GAC CCT ATG ATG GCT GAT GCC ATT GAT TTC ATG GTA GAC AGG					
699					
Pro Val Asp Pro Met Met Ala Asp Ala Ile Asp Phe Met Val Asp Arg					
	175		180		185
CTA GAA AGT TTG GGT CAG AGT GAA CTG GCT TCA AGA CTT ACC TTG AAT					
747					

PH-1064PCT-US seq.TXT

Leu Glu Ser Leu Gly Gln Ser Glu Leu Ala Ser Arg Leu Thr Leu Asn

190

195

200

TGT CAA AAT TCT TAT GTG GTA CCT CAT AAA ATT CGG GAC ATA CCT GTA
795

Cys Gln Asn Ser Tyr Val Val Pro His Lys Ile Arg Asp Ile Pro Val

205

210

215

ACT ATT ATG GAT GTG TTT GAT CAG AGT GCG CTT TCA ACT GAA GCT AAA
843

Thr Ile Met Asp Val Phe Asp Gln Ser Ala Leu Ser Thr Glu Ala Lys

220

225

230

235

GAA GAA ATG TAC AAG CTG TAT CCT AAT GCC CGA AGA GCT CAT CTG AAA
891

Glu Glu Met Tyr Lys Leu Tyr Pro Asn Ala Arg Arg Ala His Leu Lys

240

245

250

ACA GGA GGC AAT TTC CCA TAC CTG TGC AGA AGT GCA GAG GTC AAT CTT
939

Thr Gly Gly Asn Phe Pro Tyr Leu Cys Arg Ser Ala Glu Val Asn Leu

255

260

265

TAT GTA CAG ATA CAT TTG CTG CAA TTC CAT GGA ACC AAA TAC GCG GCC
987

Tyr Val Gln Ile His Leu Leu Gln Phe His Gly Thr Lys Tyr Ala Ala

270

275

280

ATT GAC CCA TCA ATG GTC AGT GCC GAG GAG CTT GAG GTG CAG AAA GGC
1035

Ile Asp Pro Ser Met Val Ser Ala Glu Glu Leu Glu Val Gln Lys Gly

285

290

295

AGC CTT GGC ATC AGC CAG GAG GAG CAG TAGTGTGTCT CTCGCTGTCA ATGATGA

PH-1064PCT-US seq.TXT

1089

Ser Leu Gly Ile Ser Gln Glu Glu Gln

300

305

GTTGACCCGG TGTGTTCTTG TATAGTCAGT GGCATCAGCA CCCGTCAGCC GGCCTTTTCC
1149

TTCAGGTTTCG TCAGGCTCAC CGGTTCTCAC TGTGTCTGGG AAGTAGGACT GATGGTCATC
1209

TTCATGACAG GCGGCATCTC CACTAAGCCT GTGTAAGTGT TCCCTCTTTG GTTTTCTTAG
1269

CTTTTGAATT TGAAGAAGTA CTTTGAAGA CTCCCATTTT AAGAACCGTG CAGATTTTGC
1329

TACCAAAAGT CTTCAACCACT GTGTTCTTAA GTGAATGTTA ATTTCTGAGG TTTGGGACTT
1389

TGTGGTGGTT TTTTCTTCT TTTCTTTTCC ATTCTTCTTT CTTTCTTTTT ATGTTGTTTG
1449

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1536

<210> 169

<211> 308

<212> PRT

<213> Homo sapiens

<400> 169

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Ser	Leu	Tyr	Asp	Ala	Gly	Pro	Arg	Ser	Ile	Arg	Cys	Pro	Leu	Ile	Phe	35	40	45	
Leu	Pro	Pro	Val	Ser	Gly	Thr	Ala	Asp	Val	Phe	Phe	Arg	Gln	Ile	Leu	50	55	60	
Ala	Leu	Thr	Gly	Trp	Gly	Tyr	Arg	Val	Ile	Ala	Leu	Gln	Tyr	Pro	Val	65	70	75	80
Tyr	Trp	Asp	His	Leu	Glu	Phe	Cys	Asp	Gly	Phe	Arg	Lys	Leu	Leu	Asp	85	90	95	
His	Leu	Gln	Leu	Asp	Lys	Val	His	Leu	Phe	Gly	Ala	Ser	Leu	Gly	Gly	100	105	110	
Phe	Leu	Ala	Gln	Lys	Phe	Ala	Glu	Tyr	Thr	His	Lys	Ser	Pro	Arg	Val	115	120	125	
His	Ser	Leu	Ile	Leu	Cys	Asn	Ser	Phe	Ser	Asp	Thr	Ser	Ile	Phe	Asn	130	135	140	
Gln	Thr	Trp	Thr	Ala	Asn	Ser	Phe	Trp	Leu	Met	Pro	Ala	Phe	Met	Leu	145	150	155	160
Lys	Lys	Ile	Val	Leu	Gly	Asn	Phe	Ser	Ser	Gly	Pro	Val	Asp	Pro	Met				

PH-1064PCT-US seq.TXT

				165					170					175			
Met	Ala	Asp	Ala	Ile	Asp	Phe	Met	Val	Asp	Arg	Leu	Glu	Ser	Leu	Gly		
			180					185					190				
Gln	Ser	Glu	Leu	Ala	Ser	Arg	Leu	Thr	Leu	Asn	Cys	Gln	Asn	Ser	Tyr		
		195					200					205					
Val	Val	Pro	His	Lys	Ile	Arg	Asp	Ile	Pro	Val	Thr	Ile	Met	Asp	Val		
	210					215					220						
Phe	Asp	Gln	Ser	Ala	Leu	Ser	Thr	Glu	Ala	Lys	Glu	Glu	Met	Tyr	Lys		
225					230					235					240		
Leu	Tyr	Pro	Asn	Ala	Arg	Arg	Ala	His	Leu	Lys	Thr	Gly	Gly	Asn	Phe		
			245						250					255			
Pro	Tyr	Leu	Cys	Arg	Ser	Ala	Glu	Val	Asn	Leu	Tyr	Val	Gln	Ile	His		
		260						265					270				
Leu	Leu	Gln	Phe	His	Gly	Thr	Lys	Tyr	Ala	Ala	Ile	Asp	Pro	Ser	Met		
	275					280						285					
Val	Ser	Ala	Glu	Glu	Leu	Glu	Val	Gln	Lys	Gly	Ser	Leu	Gly	Ile	Ser		
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Gln	Glu	Glu	Gln														
305																	

<210> 170

<211> 2560

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (202)..(1002)

<400> 170

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120
AGTGGTCGGA GCCCGCCAGT GGGCAGGCAG CTCTTGCTCA CAGGCCGCGG TGCCCAGGCC
180
GCTGGCTCTC CGCAGGGCGG A ATG GCG CTG CAA GTG GAG CTG GTA CCC ACC
231

Met Ala Leu Gln Val Glu Leu Val Pro Thr

1

5

10

GGG GAG ATC ATC CGC GTG GTT CAT CCC CAC AGG CCC TGC AAG CTT GCC
279
Gly Glu Ile Ile Arg Val Val His Pro His Arg Pro Cys Lys Leu Ala

15

20

25

PH-1064PCT-US seq.TXT

CTG GGC AGT GAC GGG GTT CGG GTG ACC ATG GAG AGT GCG CTC ACC GCC
327

Leu Gly Ser Asp Gly Val Arg Val Thr Met Glu Ser Ala Leu Thr Ala

30

35

40

CGT GAC CGG GTG GGG GTG CAG GAT TTC GTG CTG CTG GAG AAC TTC ACC
375

Arg Asp Arg Val Gly Val Gln Asp Phe Val Leu Leu Glu Asn Phe Thr

45

50

55

AGC GAG GCC GCC TTC ATC GGG AAC CTG CGG CGG CGA TTT CGG GAG AAT
423

Ser Glu Ala Ala Phe Ile Gly Asn Leu Arg Arg Arg Phe Arg Glu Asn

60

65

70

CTC ATC TAC ACC TAC ATT GGC CCC GTC CTG GTC TCT GTC AAT CCC TAC
471

Leu Ile Tyr Thr Tyr Ile Gly Pro Val Leu Val Ser Val Asn Pro Tyr

75

80

85

90

CGG GAC CTG CAG ATC TAC AGC CGG CAG CAT ATG GAG CGT TAC CGT GGC
519

Arg Asp Leu Gln Ile Tyr Ser Arg Gln His Met Glu Arg Tyr Arg Gly

95

100

105

GTC AGC TTC TAT GAA GTG CCC CCT CAC CTG TTT GCC GTG GCG GAC ACT
567

Val Ser Phe Tyr Glu Val Pro Pro His Leu Phe Ala Val Ala Asp Thr

110

115

120

GTG TAC CGA GCA CTG CGC ACG GAG CGT CGG GAC CAG GCT GTG ATG ATC
615

Val Tyr Arg Ala Leu Arg Thr Glu Arg Arg Asp Gln Ala Val Met Ile

125

130

135

PH-1064PCT-US seq.TXT

TCT GGG GAG AGC GGG GCA GGC AAG ACC GAG GCC ACC AAG AGG CTG CTG
663

Ser Gly Glu Ser Gly Ala Gly Lys Thr Glu Ala Thr Lys Arg Leu Leu

140

145

150

CAG TTC TAT GCA GAG ACC TGC CCA GCC CCC GAG CGC GGA GGT GCC GTG
711

Gln Phe Tyr Ala Glu Thr Cys Pro Ala Pro Glu Arg Gly Gly Ala Val

155

160

165

170

CGG GAC CGG CTG CTA CAG AGC AAC CCG GTG CTG GAG GCC TTT GGA AAT
759

Arg Asp Arg Leu Leu Gln Ser Asn Pro Val Leu Glu Ala Phe Gly Asn

175

180

185

GCC AAG ACC CTC CGG AAC GAT AAC TCC AGC AGG TTC GGG AAG TAC ATG
807

Ala Lys Thr Leu Arg Asn Asp Asn Ser Ser Arg Phe Gly Lys Tyr Met

190

195

200

GAT GTG CAG TTT GAC TTC AAG GGT GCC CCC GTG GGT GGC CAC ATC CTC
855

Asp Val Gln Phe Asp Phe Lys Gly Ala Pro Val Gly Gly His Ile Leu

205

210

215

AGT TAC CCC CTG GAA AAG TCA CGA GTG GTG CAC CAG AAT CAT GGG GAG
903

Ser Tyr Pro Leu Glu Lys Ser Arg Val Val His Gln Asn His Gly Glu

220

225

230

CGG AAC TTC ACA TCT TCT ACC AGC TGC TGG AGG GGG GCG AGG AGG AGA
951

Arg Asn Phe Thr Ser Ser Thr Ser Cys Trp Arg Gly Ala Arg Arg Arg

235

240

245

250

PH-1064PCT-US seq.TXT

CTC TTC GCA GGC TGG GCT TGG AAC GGA ACC CCC AGA GCT ATC TGT ACC
999

Leu Phe Ala Gly Trp Ala Trp Asn Gly Thr Pro Arg Ala Ile Cys Thr

255

260

265

TGG TGAAGGCCAG TGTGCCAAAG TCTTCTTCAT CAACGACAAG AGTGA CTGGA AGGTCTG
1058

Trp

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1118

TCGTGGCCAG CGTCCTTCAT TTGGGCAACA TCCACTTTGC TGCCAACGAG GAGAGCAATG
1178

CCCAGGTCAC CACCGAGAAC CAGCTCAAGT ATCTGAGCCC ATTCAGTATG CGGTGCCTGT
1238

TGTGAAATAC GACCGCAAGG GCTACAAGCC TCGCTCCCGG CAGCTGCTGC TCACGCCCAA
1298

CGCCGTCGTC ATCGTGGAGG ACGCCAAAGT CAAGCAGAGG ATTGATTACG CCAACCTGAC
1358

CGGAATCTCT GTCAGCAGCC TGAGCGACAG TCTTTTTGTG CTTTCATGTAC AGCGTGCGGA
1418

CAATAAGCAA AAGGGAGATG TGGTGCTGCA GAGTGACCAC GTGATTGAGA CGCTGACCAA
1478

GACAGCCCTC AGTGCCAACC GCGTGAACAG CATCAACATC AACCAGGGCA GCATCACGTT
1538

TGCAGGGGGC CCCGGCAGGG ATGGCACCAT TGA CTTCACA CCCGGCTCGG AGCTGCTCAT
1598

CACCAAGGCC AAGAACGGGC ACCTGGCTGT GGTCGCCCCA CGGCTGAATT CTCGGTGATA
1658

AAGGCGCCCA CTGGACCCTC CCAACGCCCA ATGCTTTGCT TTTCTCCTCC TCCCCTTCCC
1718

AGTTACCAA GACTCGAACT TCCAGACAGG GACCCAGGGA CACCCCGAAG CCCACCTGCA
1778

ATCTCCCACC TCCTGCCCAT CCCTCTCTTG AGGGAGCAGC AGGGGCCAGG AGCTACCCCA
1838

GGAGTGGGCC AGGCCGGGCC ACAGCAATAG GAAAGCCAGG GCCAGAGCGA GCCATGCCAG
1898

CCCTACTGCC GATGCCAAAT ATTTGAGAGA AGGGA ACTTT TGCTGAGGTT TTCTCTGAGG
1958

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2018

ACAGTGGATG TGTTTTCCCT GACTCCAGCA GGGCAAGGAA ATGTAGCCGA GAGGTTGTGT

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2078
GGGCTGGGCT CTGGTGCCCT CTTCCCTGGC CAGGACACCT CTCCTCCTGA TTCCCTTGGC
2138
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2198
CACTCTGACT TCCATCTGGG GGCTGAGACC ACCCTTGCCT GCCCCCTTCT TTCTGCCTTA
2258
AGAATGTCCT TTTAGGCTGG GCATGGTGGC TCACGCCTGT AACCCCAGCA CTTTGGGAGG
2318
CGGAGACGGG CAGATAACCT GAGGTCAGGA TTTCGAGACC AACCTGACCT ACATGGAGAA
2378
ACTCCGCCTC TGGTAAGGAT ACAAATTAG CCGGGCATGG TGGTGCACGC CTCTAATCCC
2438
AGCTGCTCGG GAGGCTGAGG CAGGAGAATC ACTTGAACCC GGAAGTGA GGTTCAGTG
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2558

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2560

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<212> PRT

<213> Homo sapiens

<400> 171

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Arg	Val	Thr	Met	Glu	Ser	Ala	Leu	Thr	Ala	Arg	Asp	Arg	Val	Gly	Val
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Gln	Asp	Phe	Val	Leu	Leu	Glu	Asn	Phe	Thr	Ser	Glu	Ala	Ala	Phe	Ile
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Gly	Asn	Leu	Arg	Arg	Arg	Phe	Arg	Glu	Asn	Leu	Ile	Tyr	Thr	Tyr	Ile
	65				70					75					80
Gly	Pro	Val	Leu	Val	Ser	Val	Asn	Pro	Tyr	Arg	Asp	Leu	Gln	Ile	Tyr
			85						90					95	
Ser	Arg	Gln	His	Met	Glu	Arg	Tyr	Arg	Gly	Val	Ser	Phe	Tyr	Glu	Val
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Pro	Pro	His	Leu	Phe	Ala	Val	Ala	Asp	Thr	Val	Tyr	Arg	Ala	Leu	Arg
		115					120					125			
Thr	Glu	Arg	Arg	Asp	Gln	Ala	Val	Met	Ile	Ser	Gly	Glu	Ser	Gly	Ala
	130					135					140				
Gly	Lys	Thr	Glu	Ala	Thr	Lys	Arg	Leu	Leu	Gln	Phe	Tyr	Ala	Glu	Thr
	145				150					155					160
Cys	Pro	Ala	Pro	Glu	Arg	Gly	Gly	Ala	Val	Arg	Asp	Arg	Leu	Leu	Gln
			165						170					175	
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Lys	Gly	Ala	Pro	Val	Gly	Gly	His	Ile	Leu	Ser	Tyr	Pro	Leu	Glu	Lys		
	210					215					220						
Ser	Arg	Val	Val	His	Gln	Asn	His	Gly	Glu	Arg	Asn	Phe	Thr	Ser	Ser		
225					230					235					240		
Thr	Ser	Cys	Trp	Arg	Gly	Ala	Arg	Arg	Arg	Leu	Phe	Ala	Gly	Trp	Ala		
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 118

Met

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 166
 Arg Pro Arg Gly Arg Lys Ala Ala Ser Pro Gly Ala Pro Arg Pro Trp
 5 10 15

CCG CGT CAC AGC ACC CAC ATG GCC TCT GGA GTG GGC GCG GCC TTC GAG
 214
 Pro Arg His Ser Thr His Met Ala Ser Gly Val Gly Ala Ala Phe Glu
 20 25 30

GAA CTG CCT CAC GAC GGC ACG TGT GAC GAG TGC GAG CCC GAC GAG GCT
 262
 Glu Leu Pro His Asp Gly Thr Cys Asp Glu Cys Glu Pro Asp Glu Ala
 35 40 45

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CCG GGG GCC GAG GAA GTG TGC CGA GAA TGC GGC TTC TGC TAC TGC CGC
310

Pro Gly Ala Glu Glu Val Cys Arg Glu Cys Gly Phe Cys Tyr Cys Arg

50

55

60

65

CGC CAT GCC GAG GCG CAC AGG CAG AAG TTC CTC AGT CAC CAT CTG GCC
358

Arg His Ala Glu Ala His Arg Gln Lys Phe Leu Ser His His Leu Ala

70

75

80

GAA TAC GTC CAC GGC TCC CAG GCC TGG ACC CCG CCA GCT GAC GGA GAG
406

Glu Tyr Val His Gly Ser Gln Ala Trp Thr Pro Pro Ala Asp Gly Glu

85

90

95

GGG GCG GGG AAG GAA GAA GCG GAG GTC AAG GTG GAG CAG GAG AGG GAG
454

Gly Ala Gly Lys Glu Glu Ala Glu Val Lys Val Glu Gln Glu Arg Glu

100

105

110

ATA GAA AGC GAG GCA GGG GAA GAG AGT GAG TCG GAG GAA GAG AGC GAG
502

Ile Glu Ser Glu Ala Gly Glu Glu Ser Glu Ser Glu Glu Glu Ser Glu

115

120

125

TCA GAG GAA GAG AGC GAG ACA GAG GAA GAG AGT GAG GAT GAG AGC GAT
550

Ser Glu Glu Glu Ser Glu Thr Glu Glu Glu Ser Glu Asp Glu Ser Asp

130

135

140

145

GAG GAG AGT GAA GAA GAC AGC GAG GAA GAA ATG GAG GAT GAG CAA GAA
598

Glu Glu Ser Glu Glu Asp Ser Glu Glu Glu Met Glu Asp Glu Gln Glu

PH-1064PCT-US seq.TXT

150

155

160

AGC GAG GCC GAA GAA GAC AAC CAA GAA GAA GGG GAA TCC GAG GCG GAG
646

Ser Glu Ala Glu Glu Asp Asn Gln Glu Glu Gly Glu Ser Glu Ala Glu

165

170

175

GGA GAA ACT GAG GCA GAA AGT GAA TTT GAC CCA GAA ATA GAA ATG GAA
694

Gly Glu Thr Glu Ala Glu Ser Glu Phe Asp Pro Glu Ile Glu Met Glu

180

185

190

GCA GAG AGA GTG GCC AAG AGG AAG TGT CCG GAC CAT GGG CTT GAT TTG
742

Ala Glu Arg Val Ala Lys Arg Lys Cys Pro Asp His Gly Leu Asp Leu

195

200

205

AGT ACC TAT TGC CAG GAA GAT AGG CAG CTC ATC TGT GTC CTG TGT CCA
790

Ser Thr Tyr Cys Gln Glu Asp Arg Gln Leu Ile Cys Val Leu Cys Pro

210

215

220

225

GTC ATT GGG GCT CAC CAG GGC CAC CAA CTC TCC ACC CTA GAC GAA GCC
838

Val Ile Gly Ala His Gln Gly His Gln Leu Ser Thr Leu Asp Glu Ala

230

235

240

TTT GAA GAA TTA AGA AGC AAA GAC TCA GGT GGA CTG AAG GCC GCT ATG
886

Phe Glu Glu Leu Arg Ser Lys Asp Ser Gly Gly Leu Lys Ala Ala Met

245

250

255

ATC GAA TTG GTG GAA AGG TTG AAG TTC AAG AGC TCA GAC CCT AAA GTA
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Ile Glu Leu Val Glu Arg Leu Lys Phe Lys Ser Ser Asp Pro Lys Val

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982		
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CAG AAA GTG ATT GCT GAT GAG GAG CAG AAG GCC CTT CAT CTA GTG GAC		
1030		
Gln Lys Val Ile Ala Asp Glu Glu Gln Lys Ala Leu His Leu Val Asp		
290	295	300
ATC CAA GAG GCA ATG GCC ACA GCT CAT GTG ACT GAG ATA CTG GCA GAC		
1078		
Ile Gln Glu Ala Met Ala Thr Ala His Val Thr Glu Ile Leu Ala Asp		
310	315	320
ATC CAA TCC CAC ATG GAT AGG TTG ATG ACT CAG ATG GCC CAA GCC AAG		
1126		
Ile Gln Ser His Met Asp Arg Leu Met Thr Gln Met Ala Gln Ala Lys		
325	330	335
GAA CAA CTT GAT ACC TCT AAT GAA TCA GCT GAG CCA AAG GCA GAG GGC		
1174		
Glu Gln Leu Asp Thr Ser Asn Glu Ser Ala Glu Pro Lys Ala Glu Gly		
340	345	350
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1225		
Asp Glu Glu Gly Pro Ser Gly Ala Ser Glu Glu Glu Asp Thr		
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1405
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1465
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1525
CCCCCATAAT ATTGTATTAC CAAACAGTAT CGCTTTGTGA GGAAGGATCT GGAATAATCT
1585
TGAAGGGAAG TCAGAGTTTT CTCCCTGCCT ATTAACAAAA ACCCAATTTT GTTCATATTG
1645
AAGCATGAAA TAAATGAGAG CAAGGTAGGG CCAAATTAAC TCTTGTGGAC AGTCCCTAAA
1705
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1765
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1825
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1885
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1945
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2005
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2065
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2125
CCTAATTTGG CTAAACGCA GTATGGGGAG AATTGTTCCC ATTCCATGTG TTCTGAATTC
2185
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2245
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2305
CTTAGTAACA GAGACACTCC TGAGGTTGGA CTCCTTGCT TTTCTCTACT TCCAAATCAC
2365
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2425
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<213> Homo sapiens

<400> 173

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			20					25					30		
Glu	Glu	Leu	Pro	His	Asp	Gly	Thr	Cys	Asp	Glu	Cys	Glu	Pro	Asp	Glu
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	50					55					60				
Arg	Arg	His	Ala	Glu	Ala	His	Arg	Gln	Lys	Phe	Leu	Ser	His	His	Leu
65					70					75					80
Ala	Glu	Tyr	Val	His	Gly	Ser	Gln	Ala	Trp	Thr	Pro	Pro	Ala	Asp	Gly
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Glu	Gly	Ala	Gly	Lys	Glu	Glu	Ala	Glu	Val	Lys	Val	Glu	Gln	Glu	Arg
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Glu	Ile	Glu	Ser	Glu	Ala	Gly	Glu	Glu	Ser	Glu	Ser	Glu	Glu	Glu	Ser
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Glu	Ser	Glu	Glu	Glu	Ser	Glu	Thr	Glu	Glu	Glu	Ser	Glu	Asp	Glu	Ser
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Glu	Ser	Glu	Ala	Glu	Glu	Asp	Asn	Gln	Glu	Glu	Gly	Glu	Ser	Glu	Ala
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Glu	Gly	Glu	Thr	Glu	Ala	Glu	Ser	Glu	Phe	Asp	Pro	Glu	Ile	Glu	Met
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Glu	Ala	Glu	Arg	Val	Ala	Lys	Arg	Lys	Cys	Pro	Asp	His	Gly	Leu	Asp
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Leu	Ser	Thr	Tyr	Cys	Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys
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Pro	Val	Ile	Gly	Ala	His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu
225					230					235					240
Ala	Phe	Glu	Glu	Leu	Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala
				245					250					255	
Met	Ile	Glu	Leu	Val	Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys
		260						265					270		
Val	Thr	Arg	Asp	Gln	Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys
		275					280					285			
Val	Gln	Lys	Val	Ile	Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val
	290					295					300				
Asp	Ile	Gln	Glu	Ala	Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala
305					310					315					320
Asp	Ile	Gln	Ser	His	Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala
				325					330					335	
Lys	Glu	Gln	Leu	Asp	Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu
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